

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
7 December 2000 (07.12.2000)

PCT

(10) International Publication Number
WO 00/73469 A2

(51) International Patent Classification⁷: C12N 15/54,
9/12, 15/11, 5/12, C07K 16/40, A61K 38/00, G01N 33/68

(21) International Application Number: PCT/US00/14842

(22) International Filing Date: 26 May 2000 (26.05.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/136,503 28 May 1999 (28.05.1999) US

(71) Applicant (for all designated States except US): SUGEN,
INC. [US/US]; 230 East Grand Avenue, South San Fran-
cisco, CA 94080 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): PLOWMAN, Gre-
gory, D. [US/US]; 4 Honeysuckle Lane, San Carlos, CA
94070 (US). MARTINEZ, Ricardo [US/US]; 984 Cartier
Lane, Foster City, CA 94404 (US). WHYTE, David
[US/US]; 2623 Barclay Way, Belmont, CA 94002 (US).
SUDERSANAM, Sucha [US/US]; 20 Corte Patencio,
Greenbrae, CA 94904 (US).

(74) Agents: WARBURG, Richard, J. et al.; Brobeck, Phleger
& Harrison LLP, 12390 El Camino Real, San Diego, CA
92130 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE,
DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID,
IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL,
PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— Without international search report and to be republished
upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypep-
tides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

WO 00/73469 A2

DESCRIPTION
PROTEIN KINASES

FIELD OF THE INVENTION

5 The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10 The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

 Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key
15 biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

 Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:
20 cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the
25 etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

 The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism
30 includes changes in the catalytic properties (V_{max} and K_m) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple alignment of the sequences in the catalytic domain of protein kinases and subsequent
20 parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

25 We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

30 Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungal-specific kinases, and a family designated “other” to represent several smaller families. In addition, we designate an “atypical” family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5 The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

 The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca²⁺/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain
10 kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

 CMGC group kinases are “proline-directed” enzymes phosphorylating residues
15 that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

 The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as
20 transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

 Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the
25 yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close
30 homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD_sp, YGR262_sc) kinases, and others that are “unique” and don’t cluster into any obvious family.

SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting

SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
5 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides
conjugated to each other, including DNA and RNA, that is isolated from a natural source
10 or that is synthesized. The isolated nucleic acid of the present invention is unique in the
sense that it is not found in a pure or separated state in nature. Use of the term "isolated"
indicates that a naturally occurring sequence has been removed from its normal cellular
(*i.e.*, chromosomal) environment. Thus, the sequence may be in a cell-free solution or
placed in a different cellular environment. The term does not imply that the sequence is
15 the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at
least) of non-nucleotide material naturally associated with it, and thus is distinguished
from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the
specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of
20 the total DNA or RNA present in the cells or solution of interest than in normal or
diseased cells or in the cells from which the sequence was taken. This could be caused by
a person by preferential reduction in the amount of other DNA or RNA present, or by a
preferential increase in the amount of the specific DNA or RNA sequence, or by a
combination of the two. However, it should be noted that enriched does not imply that
25 there are no other DNA or RNA sequences present, just that the relative amount of the
sequence of interest has been significantly increased. The term "significant" is used to
indicate that the level of increase is useful to the person making such an increase, and
generally means an increase relative to other nucleic acids of about at least 2 fold, more
preferably at least 5 to 10 fold or even more. The term also does not imply that there is no
30 DNA or RNA from other sources. The other source DNA may, for example, comprise
DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term
distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6 -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
5 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
10 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional
15 derivatives thereof as described herein. For sequences for which the full-length sequence
is not given, the remaining sequences can be determined using methods well-known to
those in the art and are intended to be included in the invention. In certain aspects,
polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide
can be encoded by a full-length nucleic acid sequence or any portion of the full-length
20 nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By
“functional” domain is meant any region of the polypeptide that may play a regulatory or
catalytic role as predicted from amino acid sequence homology to other proteins or by the
presence of amino acid sequences that may give rise to specific structural conformations
(*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but
25 not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from
the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
30 NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID
NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID

NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID
5 NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID
NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID
10 NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID
NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID
15 NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding
20 full-length amino acid sequence, or fragments thereof. A sequence that is substantially
similar to a sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
30 NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ

ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 or portions of or the entire corresponding full-length amino acid sequences.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402), Blast2 (Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) *J. Mol. Biol.* 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
5 NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID
10 NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will
15 have at least 75% identity (preferably 90%, more preferably at least 95% and most
preferably 99-100%) to the sequence selected from the group consisting of those set forth
in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
20 NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
25 NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID
NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID
NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID
NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
30 NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID

NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID
NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID
5 NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c)
10 hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes
a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an
amino acid sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
15 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
20 NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
25 NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
30 NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
5 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
10 NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
15 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
20 NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
25 ID NO:242, except that it lacks one or more, but not all, of a domain selected from the
group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a
coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-
terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a
polypeptide having an amino acid sequence selected from the group consisting of those set
30 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
5 NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
10 NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
15 NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95%
and most preferably 99-100%) to the sequence selected from the group consisting of those
20 set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ
ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ
ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ
ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ
ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ
25 ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ
ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ
ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ
ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ
ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ
30 ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ
ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ
ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of

those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID
NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID
NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID
NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID
5 NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID
NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID
NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID
NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID
10 NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID
NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID
NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID
NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID
NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID
15 NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID
NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID
NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID
NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID
20 NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID
NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID
NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID
NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID
NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
25 NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino
acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence
selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
30 SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
5 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
10 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
15 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at
20 least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-
100%) to the sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
30 NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
5 NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
10 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under
15 highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally
occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
20 NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
25 NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
30 NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) *J. Biol. Chem.* 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further,
10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate
20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine
25 amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of
30 the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

domain may play a regulatory role is PAK3 which contains a heterotrimeric G_b subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic α -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein-protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).
5 Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of
10 the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein
15 database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these
20 methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the
25 protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of
30 the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4 , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

5 The term “vector” relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding
10 a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term “transfecting” defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field,
15 detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term “promoter” as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes,
20 the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

25 In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19,
30 SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ
ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID
NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51,
SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ
ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID
NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67,
SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ
ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID
NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83,
SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ
ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID
NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99,
SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104,
SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,
SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114,
SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119,
SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes
an amino acid sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
5 NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
15 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.

25 In particular, a unique nucleic acid region is preferably of mammalian origin and preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe
contains a nucleotide base sequence that will hybridize to a sequence selected from the
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the
genomic regulatory elements, or may be under the control of exogenous regulatory
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence. By "fragment," is meant an amino acid sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (e.g., in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5 In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, 10 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, 15 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, 20 SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, 25 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, 30 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242 where the domain is selected from the group consisting of an N-terminal domain,
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in the art. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the polypeptide may be synthesized using an automated polypeptide synthesizer. The isolated, enriched, or purified kinase polypeptide is preferably selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By “recombinant kinase polypeptide” is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By “specific binding affinity” is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term “specific binding affinity” describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term “polyclonal” refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

“Monoclonal antibodies” are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term “antibody fragment” refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

5 An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

10 Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may
15 be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

20 In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
25 NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
30 NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID

NO:242. The binding agent is preferably a purified antibody that recognizes an epitope
present on a kinase polypeptide of the invention. Other binding agents include molecules
that bind to kinase polypeptides and analogous molecules that bind to a kinase
15 polypeptide. Such binding agents may be identified by using assays that measure kinase
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a
kinase polypeptide of the invention or an equivalent sequence. The method involves
identifying the novel polypeptide in human cells using techniques that are routine and
20 standard in the art, such as those described herein for identifying the kinases of the
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)
measuring the activity of said polypeptide; and (c) determining whether said substance
modulates the activity of said polypeptide.

20 The term "modulates" refers to the ability of a compound to alter the function of a
kinase of the invention. A modulator preferably activates or inhibits the activity of a
kinase of the invention.

The term "activates" refers to increasing the cellular activity of the kinase. The
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is
25 preferably the interaction with a natural binding partner.

The term "modulates" also refers to altering the function of kinases of the
invention by increasing or decreasing the probability that a complex forms between the
kinase and a natural binding partner. A modulator preferably increases the probability that
such a complex forms between the kinase and the natural binding partner, more preferably
30 increases or decreases the probability that a complex forms between the kinase and the
natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term “complex” refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term “natural binding partner” refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term “contacting” as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
10 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
15 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change
in cell phenotype or the interaction between said polypeptide and a natural binding
partner.

The term “expressing” as used herein refers to the production of kinases of the
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic
20 acid vector is transfected into cells using well known techniques in the art as described
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal
condition by administering to a patient in need of such treatment a substance that
modulates the activity of a polypeptide selected from the group consisting of SEQ ID
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term “preventing” refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5 The term “treating” refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

10 The term “therapeutic effect” refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating efficacy against abnormal conditions can be identified as described herein.

15 The term “abnormal condition” refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in normal cell cycle progression through mitosis and meiosis.

20 Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

25 Abnormal differentiation conditions include, but are not limited to neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

30 Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the protein kinases could lead to cell immortality or premature cell death.

The term “aberration”, in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term “administering” relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the complements of the sequences and fragments; and (b) detecting the presence or amount of the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, organ transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative stress-related neurodegenerative disorders, metabolic disorder including diabetes, reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding

full-length amino acid sequence, or a functional derivative thereof. Hybridization conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

“Amplification” as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722
10 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris
15 *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432
30 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:

1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).

Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
15 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
20 NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
25 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
30 NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include, but are not limited to, those discussed previously.

The term “comparing” as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine these discrepancies in sequences are well-known to one of ordinary skill in the art. The “control” nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides, assays utilizing such polypeptides, and methods relating to all of the foregoing. The present invention is based upon the isolation and characterization of new kinase polypeptides. The polypeptides and nucleic acids may be produced using well-known and standard synthesis techniques when given the sequences presented herein.

I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the herein-described isolated nucleic acid molecules. The degeneracy of the genetic code permits substitution of certain codons by other codons that specify the same amino acid and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide or polynucleotide may be used in this regard, provided that its addition, deletion or substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded
by the nucleotide sequence. For example, the present invention is intended to include any
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or
its derivative. Moreover, the nucleic acid molecule of the present invention may, as
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity
25 to promote secretion and/or processing of heterologous proteins encoded by foreign
nucleic acid sequences fused thereto, for example. All variations of the nucleotide
sequence of the kinase genes of the invention and fragments thereof permitted by the
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with
30 codons other than degenerate codons to produce a structurally modified polypeptide, but
one which has substantially the same utility or activity as the polypeptide produced by the
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5 Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.
10 Therefore, these nucleic acid molecules are also part of the invention.

 The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore
15 presumably define new protein kinase groups.

 Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

20 II. Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

 A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,
25 Sambrook, Fritsch, & Maniatis, eds., 1989).

 In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain
30 reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

5 A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the
10 regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of
15 transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and
20 polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence
25 encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the
30 promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include γ gt10, γ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ , the *bla* promoter of the β -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the α -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ζ -28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

promoters are reviewed by Glick (Ind. Microbiol. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184, π VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kiado, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
 SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
 SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
 5 SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
 SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
 SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
 10 SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
 NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of
 these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-
 15 terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are
 provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI,
 CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant
 number of protein kinases that do not belong to any of the known groups, and therefore
 20 presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1,
 Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein 25 Kinases

The present invention relates to an antibody having binding affinity to a kinase of
 the invention. The polypeptide may have an amino acid sequence selected from the group
 consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
 ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
 30 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
 ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the polypeptide not provided in the sequences above, but that is present in the full-length sequence of the polypeptide and that is easily obtained using methods standard in the art. Further, the antibody may bind specifically to particular domains of one or more of the kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to a kinase or kinase domain of the invention. Such an antibody may be isolated by comparing its binding affinity to a kinase of the invention with its binding affinity to other polypeptides. Those that bind selectively to a kinase of the invention would be chosen for use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspiczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S.
20 Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzyldene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzyldene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune, neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatin, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

Tumor associated: Mok (SEQ ID NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

Neuronal restricted: CAMKKB (SEQ ID NO:66)

Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

VIII. Transgenic Animals.

A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (e.g., the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (Experientia 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO₂ asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, Cell 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is
10 precipitated with CaPO_4 and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic
25 acid molecule into a cell. Gene transfer is commonly performed to enable the expression of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express
5 a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid
10 sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or
15 modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

20 X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by
25 reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of
30 the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

15

Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

20

25

Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

30

with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

| | ID# | ID# | Parent | 5' primer | 3' primer |
|----|-----|-----|-------------------------|------------------------------|---------------------------------|
| sp | na | aa | Sequence | Sequence* | Sequence* |
| H | 33 | 153 | 2R22-5-11 | GAGATCGRNTTYAARGA RTTYGA | TGTCACNCCNAGNSWCCAN AYRTT |
| M | 81 | 200 | 5R57_10_2_ m TESK2_m | GCTGCTGGACAGTGACT TGTATTT | GAAAGCAAAGCCTTCACAC CTT |
| H | 67 | 187 | 5R69_17_2_h | CTCTCACCTCAGGAACT GG | GCTTGCGGATCTTCTCA |
| H | 46 | 166 | SGK309_h | GACATCCTGCCGGCCAA CTACG | CGGCCCTGGAGCTGCATCA CTA |
| M | 67 | 228 | 5R72_16_2_h | TGCGCGACACCATTGAC CAG | CTCAGGGCTTACATACAGA G |
| H | 45 | 165 | 5R72_8_2_h | AAAGGAGAACTACATTT TGAAAAT | CTTCATCATCTCTAATACAT TGGTTGG |
| H | 41 | 161 | Z36720 | CAAATTAAGATCATTGA CTTTGGG | GGAAACAAAGTCCTTGGCC TC |
| H | 115 | 234 | AL031652 - Pak6 | GTGGACATCTGGTCCCT CG | GTAGGTCCTTCACTCTTGG AG |

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

10

Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

15

PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

| Database | Database Date |
|--------------------|---------------|
| LifeGold templates | Feb 2000 |
| LifeGold compseqs | Feb 2000 |
| LifeGold compseqs | Mar 2000 |
| LifeGold compseqs | Apr 2000 |
| LifeGold fl | Feb 2000 |
| LifeGold flt | Apr 2000 |
| NCBI human Ests | May 2000 |
| NCBI murine Ests | May 2000 |
| NCBI nonredundant | May 2000 |

5 Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

| Database | Number of entries | Database Date |
|------------------|-------------------|---------------|
| Celera v. 1-5 | 5,306,158 | Jan 19/00 |
| Celera v. 6-10 | 4,209,980 | Mar 24/00 |
| Celera v. 11-14 | 7,222,425 | Apr 24/00 |
| Celera v. 15 | 243,044 | May 14/00 |
| HGP all Genescan | 25,885 | Apr 04/00 |
| HGP; Phase 0 | 4,944 | May 04/00 |
| HGP; Phase 1 | 28,478 | May 05/00 |
| HGP; Phase 2 | 1,508 | May 04/00 |
| HGP; Phase 3 | 9,971 | May 05/00 |

Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the *evc* (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

Human 5R79-46-1_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- κ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceded by the sequence "RGLLAPGDPPCPPNPAPATPPSSRLPTLFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324_h orthologue of W30246_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP_057440) used for the Smith-Waterman query): N-term from Incyte 6010175_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175_2 , Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides 1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

15 Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015_m (SEQ ID NO: 42, SEQ ID NO:162)

tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 8. Isoforms for R19772

| Kestrl Name | Kestrl AA Acc # | Isoform type | Source | Description* |
|-------------|--------------------|-----------------|--------------------|-----------------------------------|
| Trad (Duet) | R19772 | B | Skeletal muscle | Deletion of K at 124 |
| | | | | Deletion of Q at 616 |
| | | | | Substitution of E for G at 762 |
| | | C | Skeletal muscle | Deletion of K at 124 |
| | | | | Deletion of Q at 616 |
| | | | | Substitution of E for G at 762 |

| | | | | |
|--|--|---|------------|-----------------------------|
| | | | | Deletion of 32 aa (160-191) |
| | | D | Lung tumor | Deletion of Q at 616 |
| | | | | Deletion of 32 aa (160-191) |
| | | E | Lung tumor | Deletion of Q at 616 |
| | | | | Deletion of 32 aa (160-191) |

* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5 Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10 Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15 Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20 Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

25 Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31 kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478_m (SEQ ID NO:80, SEQ ID NO:199)

Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 9. Isoforms for AA232253

| Kestrl Name | Kestrl AA Acc # | Isoform type | Description* |
|-------------|-----------------|--------------|--|
| MLK4 | AA232253 | MLK4 | Substitution of C for W at 346 |
| | | MLK4B | Different Cterm (332-800); seq in MLK4B is as shown in * |

* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSNNGEGHGMNPSLQAMMLMGFGDI
FSMNKAGAVMHSGMQINMQAKQNSS
KTTSKRGRGKKVNMALGFSDFDLSEGDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

Human SGK022 orthologue of AA060026_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence 1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP_h 6921333_9; removed intron (146-893) predicted from blastx analysis.

Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG_040010.

Human orthologue of AA671275_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

5 The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

10 The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

| Prov. SEQ ID NO: (na) | Prov. SEQ ID NO: (aa) |
|-----------------------|-----------------------|
| 160 | 196 |
| 213 | 214 |
| 215 | 216 |
| 122 | 126 |
| 119 | 123 |
| 148 | 184 |
| 4 | 20 |
| 7 | 23 |
| 205 | 206 |
| 14 | 30 |
| 15 | 31 |
| 35 | 56 |
| 42 | 63 |
| 51 | 72 |
| 44 | 65 |
| 77 | 91 |

| | |
|-----|-----|
| 78 | 92 |
| 79 | 93 |
| 80 | 94 |
| 157 | 193 |

Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). “Kinase Domain Start”, “Kinase Domain End”, “Profile Start” and “Profile End” refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a “Profile Start” of 1 and a “Profile End” of 261. The boundaries of the catalytic domain within the overall protein are noted in the “Kinase Domain Start” and “Kinase Domain End” columns.

The following abbreviations were used for kinases:

| | |
|------|--|
| ASK | Apoptosis signal-regulating kinase |
| CaMK | Ca ²⁺ /calmodulin-dependent protein kinase |
| CCRK | Cell cycle-related kinase |
| CDK | Cyclin-dependent kinase |
| CK | Casein kinase |
| DAPK | Death-associated protein kinase |
| DM | myotonic dystrophy kinase |
| Dyrk | dual-specificity-tyrosine phosphorylating-regulated kinase |
| GAK | Cyclin G-associated kinase |
| GRK | G-protein coupled receptor |
| GuC | Guanylate cyclase |
| HIPK | Homeodomain-interacting protein |
| IRAK | Interleukin-1 receptor-associated kin |
| MAPK | Mitogen activated protein kinase |
| MAST | Micotubule-associated STK |
| MLCK | Myosin-light chain kinase |
| MLK | Mixed lineage kinase |
| NIMA | NimA-related protein kinase |
| PKA | cAMP-dependent protein kinase |
| RSK | Ribosomal protein S6 kinase |
| RTK | Receptor tyrosine kinase |

| | |
|-----|---|
| SGK | Serum and glucocorticoid-regulated kinase |
| STK | serine threonine kinase |
| ULK | UNC-51-like kinase |

The following abbreviations were used for species

| | |
|-----|---|
| H | Human |
| M | Murine |
| R | Rat |
| FV | Fowlpox virus |
| MT | <i>M. thermoautotrophicum</i> |
| CE | <i>Caenorhabditis elegans</i> |
| DM | <i>Drosophila melanogaster</i> |
| OS | <i>Oryza sativa</i> |
| SP | <i>Schizosaccharomyces pombe</i> |
| TP | <i>Tetrahymena pyriformis</i> |
| PI | <i>Petunia inflata</i> |
| NC | <i>Neurospora crassa</i> |
| MSV | <i>Medicago sativa</i> |
| MSV | Moloney murine sarcoma virus |
| SA | <i>Squalus acanthias</i> |
| CS | <i>Cucumis sativus</i> |
| GM | <i>Glycine max</i> |
| LL | <i>Lilium longiflorum</i> |
| TV | <i>Trichomonas vaginalis</i> |
| MP | <i>Mycoplasma pneumoniae</i> |
| DD | <i>Dictyostelium discoideum</i> |
| SC | <i>Saccharomyces cerevisiae</i> |
| MT | <i>Methanobacterium thermoautotrophicum</i> |

Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program (www.ch.embnet.org/software/COILS_form.html). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind (www.at.embnet.org/embnet/tools/bio/PESTfind/). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

Identification of potential coiled-coil domains and PEST domains in N34132

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

| Coiled-coil Region | Amino acid range | Length (aa) |
|--------------------|------------------|-------------|
| 1 | 124-147 | 24 |
| 2 | 437-451 | 15 |
| 3 | 495-526 | 32 |
| 4 | 1,723-1,749 | 27 |

Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

| PEST Region | Score | Amino acid range | Amino Acid Length |
|-------------|--------|------------------|-------------------|
| 1 | + 4.91 | 54-95 | 42 |
| 2 | +11.4 | 537-570 | 34 |
| 3 | +31.08 | 1293-1304 | 12 |
| 4 | +10.15 | 1543-1565 | 23 |
| 5 | + 6.17 | 1698-1732 | 35 |

EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map (http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at

5 http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above,

10 Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the

15 entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline

20 (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

Results

25 The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with

30 chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

EXAMPLE 3: Generation of Specific Immunoreagents

Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

| Clone Name | SEQ ID NO (aa) | Peptide Sequence | Amino Location |
|------------|----------------|------------------|----------------|
| AA8256850 | 124 | KSRDNSRDSSQSEND | 339-353 |
| | | TEKLKRSQDLPREPLP | 372-386 |
| | | RGWRPYDIHS | 223-232 |
| 5R79-46-1 | 126 | FEGPRRNKEVMYK | 224-236 |
| | | KDDYNETVHKKTE | 451-463 |
| | | GTHPKDRNVEKLQ | 541-553 |
| | | EVSKYQEYTNELQET | 643-657 |
| AA256100 | 129 | IDDTSNFDDFPESDI | 405-419 |
| | | TEPDYKSKDWVFL | 427-439 |
| | | EEKKLRRSQHARKET | 61-75 |
| AA210825 | 130 | SNKDTLRKRHYWRLD | 507-521 |
| | | RHTTRKSSTTLRE | 488-500 |
| | | FQNNTTNRYYKEIPL | 528-542 |
| | | GKHRKTGRDVAVK | 668-680 |
| | | FPTKQESQLRNE | 687-698 |

| | | | |
|-----------|-----|-----------------|-----------|
| AA316804 | 132 | ESHVHQEPSKRIPS | 239-252 |
| | | HTKRKSSTMVKEGW | 409-422 |
| | | PSDLDERDEEAVK | 375-388 |
| | | SPGQGKDHKDLSTSI | 543-557 |
| R47805 | 143 | EPVGRWDQDYDRAVL | 44-58 |
| | | KPKGPGGKRGHKRLI | 325-339 |
| | | PTDVAQLPSRVPRDA | 219-233 |
| AA234451 | 167 | DPFDWEKTGNDGSLT | 293-307 |
| | | HPRPQEKDVWEE | 374-385 |
| | | RENTDEVFPDEQLSD | 340-354 |
| | | RSEITQPDRDIPLVR | 427-441 |
| AA460132 | 180 | LKSYSTSSKKARPVL | 222-236 |
| | | KKLDEVRLRGRKRS | 237-251 |
| | | ETEKTAQGLSNLAKT | 131-145 |
| N34132 | 183 | SGRRRRPTKSKGSKS | 1848-1862 |
| | | PGTAPSKPPLTKAPV | 1474-1488 |
| | | VSDTQPKAPGIDD | 1365-1378 |
| | | AHSLDKTSHSSTTGL | 1253-1267 |
| 5R69-17-2 | 187 | GTTREKTDRVKST | 178-190 |
| | | HSEAPELHGKIRSSN | 138-152 |
| | | DETVTPPQFSIV | 87-98 |
| | | QYDVKSEIYS | 204-213 |
| AA278842 | 206 | TVDPEKSVRDQAFKA | 515-529 |
| | | DSSTADRWDDEDWGS | 637-651 |
| | | SVSEDPTQLEEVEKD | 539-553 |
| AA836348 | 232 | NAPTKRPRSSTVTEA | 323-337 |
| | | LDSEEDYYTPQKVDV | 514-528 |
| | | GDKASYRQPKHVEKL | 409-423 |

EXAMPLE 4. Expression analysis of Novel Mammalian Protein KinasesGENE EXPRESSION ANALYSIS

Tissue Arrays

“cDNA libraries” derived from a variety of sources were immobilized onto nylon
5 membranes and probed with ³²P-labeled cDNA fragments derived from the gene(s) of
interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to
generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at
each end. An oligo dT primer containing a specific sequence (CDS:

10 AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at
the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV
RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when
it adds additional C residues. If a primer (SMII:

AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G:

15 AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals
to the added Cs and the MMLV recognizes the rest of the primer sequence as template and
continues transcription. As a result, the synthesized cDNAs contain specific sequence tags
at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same
sequence (CDS and SMII) it is referred to as “symmetric.” When the 5' end is tagged
20 with a different sequence than the 3' end (CDS and ML2G) is referred to as “asymmetric”
A double-stranded “cDNA library “ is then generated by PCR amplification using the
3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2:
AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified “cDNA libraries” were manually arrayed onto nylon membranes
25 with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and
cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech)
and hybridized with ³²P labeled probes generated by random hexamer priming of cDNA
fragments corresponding to the genes of interest. After washing, the blots were exposed to
phosphorimaging cassettes and the intensity of the signal was quantified. The amount of
30 the DNA on the arrays was also quantified by treating non-denatured or denatured arrays
with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2
minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

5 Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: “Tissue”: tissue type of the cDNA; “Tumor sym”, indicates that the tissue is derived from a tumor, “sym” refers to the fact that the 5’ and 3’ primers used to make the sample are the same; “Normal Sym”, indicates normal tissue was used to make the sample, with symmetric primers as described above; “Tumor lo”, indicates that primary tumor tissue was used to make the cDNA; “Tumor cells”, indicates that these cDNA samples were made from cultured tumor cells; “Normal”, indicates that these samples are derived from normal tissue or cell lines; “Endos”, indicates that these samples are derived from endothelium-related tissue sources; “p53” refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AI086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

5

EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

15

Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

20

EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

25

Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms “comprising”, “consisting essentially of” and “consisting of” may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. ... An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
5 NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
10 NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
15 NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
20 NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
25 NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

30 (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

(d) encodes a kinase polypeptide having an amino acid sequence

selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
5 SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
10 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
15 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
20 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
25 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more,
but not all, of a domain selected from the group consisting of an N-terminal domain, a
catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region,
a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or promoter effective to initiate transcription in a host cell.

4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of
5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
10 SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
15 SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
25 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

30

7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
5 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
10 NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
15 NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
20 NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
25 NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
5 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
10 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
15 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
20 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090, N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, 15 AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ

ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

5 NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID
NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
10 NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,
5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242 with a test substance;

(b) measuring the activity of said polypeptide; and

(c) determining whether said substance modulates the activity of said

25 polypeptide.

30. A method for identifying a substance that modulates kinase activity in a
cell comprising:

(a) expressing a kinase polypeptide in a cell, wherein said polypeptide
is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID
30 NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
5 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID
10 NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID
15 NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
20 NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

- (b) adding a test substance to said cell; and
- (c) monitoring a change in cell phenotype or the interaction between
said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) contacting said sample with a nucleic acid probe which hybridizes
5 under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
10 SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
15 SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
20 SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
25 SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
30 SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

(b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

Table 1

| Gen Name | SP | Prov | Seq ID | NA | Prov | Seq ID | AA | SEQ ID | # aa | SEQ ID | # aa | Family | Group | Length | NA | Length | AA | ORF | Start | ORF | End | ORF | Length | DNA Repeats | CHR Localization |
|---------------------|----|------|--------|----|------|--------|------|--------|------|--------|------|----------|------------|--------|------|--------|------|-----|-------|------|------|------|--------|------------------|------------------|
| XGB117 h BARK2 h | H | 1 | 1 | 1 | 1 | 1 | 1 | 122 | 122 | 122 | 122 | AGC | GRK | 287 | 287 | 689 | 689 | 1 | 2054 | 2054 | 2054 | 2054 | 2054 | x | 22q11 |
| AA144574 m BARK2 m | M | 1 | 17 | 1 | 17 | 1 | 1 | 123 | 123 | 123 | 123 | AGC | GRK | 1368 | 1368 | 318 | 318 | 2 | 1135 | 1135 | 1135 | 1135 | 1135 | x | NA |
| AA228850 h | H | 140 | 178 | 3 | 178 | 3 | 178 | 124 | 124 | 124 | 124 | AGC | M3C11.1 ce | 1768 | 1768 | 419 | 419 | 8 | 1264 | 1264 | 1264 | 1264 | 1264 | 285-304 | NA |
| AA980857 h | H | 11 | 27 | 4 | 27 | 4 | 27 | 125 | 125 | 125 | 125 | AGC | M3C11.1 ce | 3224 | 3224 | 414 | 414 | 65 | 1306 | 1306 | 1306 | 1306 | 1306 | x | 4p16.1 |
| SG79451 h TBK1 h | H | 207 | 208 | 5 | 208 | 5 | 208 | 126 | 126 | 126 | 126 | AGC | M3C11.1 ce | 3013 | 3013 | 729 | 729 | 83 | 2278 | 2278 | 2278 | 2278 | 2278 | x | NA |
| AA305176 h | H | 42 | 1820 | 6 | 1820 | 6 | 1820 | 127 | 127 | 127 | 127 | AGC | NDR | 582 | 582 | 329 | 329 | 53 | 1038 | 1038 | 1038 | 1038 | 1038 | x | 10p11.2 |
| AA116841 m | M | 42 | 1820 | 7 | 1820 | 7 | 1820 | 128 | 128 | 128 | 128 | AGC | NDR | 582 | 582 | 329 | 329 | 53 | 1038 | 1038 | 1038 | 1038 | 1038 | x | NA |
| AA238100 h | H | 3 | 19 | 8 | 19 | 8 | 19 | 129 | 129 | 129 | 129 | AGC | NDR | 484 | 484 | 64 | 64 | 88 | 1477 | 1477 | 1477 | 1477 | 1477 | x | 12q11 |
| AA210825 h | H | 5 | 21 | 9 | 21 | 9 | 21 | 130 | 130 | 130 | 130 | AGC | PKC | 3263 | 3263 | 978 | 978 | 117 | 3050 | 3050 | 3050 | 3050 | 3050 | x | 18q13-q13.3 |
| AA127299 h | H | 203 | 204 | 10 | 204 | 10 | 204 | 131 | 131 | 131 | 131 | AGC | PKC | 315 | 315 | 105 | 105 | 1 | 315 | 315 | 315 | 315 | 315 | x | NA |
| AA316804 h EPK2 | H | 6 | 22 | 11 | 22 | 11 | 22 | 132 | 132 | 132 | 132 | AGC | PKC | 2873 | 2873 | 860 | 860 | 1 | 2870 | 2870 | 2870 | 2870 | 2870 | x | 2p21 |
| NA2050 h PKNbeta | H | 8 | 24 | 12 | 24 | 12 | 24 | 133 | 133 | 133 | 133 | AGC | PKC | 2870 | 2870 | 859 | 859 | 1 | 2867 | 2867 | 2867 | 2867 | 2867 | 2221-2280 | NA |
| AI021023 m PKNbeta | M | x | x | 13 | x | 13 | x | 134 | 134 | 134 | 134 | AGC | PKC | 295 | 295 | 205 | 205 | 2 | 816 | 816 | 816 | 816 | 816 | 595-838 | CHR17 |
| W19102 h | H | 12 | 28 | 14 | 28 | 14 | 28 | 135 | 135 | 135 | 135 | AGC | SGK | 1155 | 1155 | 384 | 384 | 1 | 1152 | 1152 | 1152 | 1152 | 1152 | x | 12q12-q13.1 |
| AA769563 h RPS6K1 | H | 0 | 25 | 15 | 25 | 15 | 25 | 136 | 136 | 136 | 136 | AGC | SGK | 1410 | 1410 | 469 | 469 | 1 | 1407 | 1407 | 1407 | 1407 | 1407 | x | Xq21.1 |
| AA876890 h RSK4 | H | 10 | 26 | 16 | 26 | 16 | 26 | 137 | 137 | 137 | 137 | AGC | SGK | 2238 | 2238 | 745 | 745 | 1 | 2235 | 2235 | 2235 | 2235 | 2235 | x | 7q21.1 |
| AA215680 h | H | 227 | 228 | 17 | 228 | 17 | 228 | 138 | 138 | 138 | 138 | AGC | SGK | 1650 | 1650 | 549 | 549 | 1 | 1647 | 1647 | 1647 | 1647 | 1647 | 767-786 | 14q24.3 |
| SGK h | H | x | x | 18 | x | 18 | x | 139 | 139 | 139 | 139 | AGC | SGK | 1290 | 1290 | 431 | 431 | 1 | 1293 | 1293 | 1293 | 1293 | 1293 | 658-683 | 8q21-q22 |
| AA107315 m | M | 13 | 29 | 19 | 29 | 19 | 29 | 140 | 140 | 140 | 140 | AGC | SGK | 2432 | 2432 | 430 | 430 | 75 | 1364 | 1364 | 1364 | 1364 | 1364 | 1804-1830 | NA |
| AA109508 m | M | 13 | 29 | 20 | 29 | 20 | 29 | 141 | 141 | 141 | 141 | AGC | SGK | 1346 | 1346 | 244 | 244 | 2 | 733 | 733 | 733 | 733 | 733 | x | NA |
| AA887183 h SGK3 SGK | H | 18 | 32 | 21 | 32 | 21 | 32 | 142 | 142 | 142 | 142 | AGC | SGK | 2250 | 2250 | 448 | 448 | 36 | 1047 | 1047 | 1047 | 1047 | 1047 | x | 3p14.3 |
| RA7605 h PTRBL | H | 131 | 107 | 22 | 107 | 22 | 107 | 143 | 143 | 143 | 143 | Atypical | AG | 1050 | 1050 | 349 | 349 | 1 | 1047 | 1047 | 1047 | 1047 | 1047 | x | 1p31.1-p32.3 |
| SGK324 h | H | 33 | 54 | 23 | 54 | 23 | 54 | 144 | 144 | 144 | 144 | CAMK | AMPK | 2310 | 2310 | 440 | 440 | 420 | 1738 | 1738 | 1738 | 1738 | 1738 | 208-227 | NA |
| W20246 m SGK324 m | M | x | x | 24 | x | 24 | x | 145 | 145 | 145 | 145 | CAMK | CAMK | 3240 | 3240 | 692 | 692 | 7 | 2082 | 2082 | 2082 | 2082 | 2082 | x | NA |
| AA197883 m | M | 38 | 57 | 25 | 57 | 25 | 57 | 146 | 146 | 146 | 146 | CAMK | CAMK | 1248 | 1248 | 297 | 297 | 1 | 891 | 891 | 891 | 891 | 891 | x | NA |
| AA172300 h DRAK2 | H | 37 | 58 | 26 | 58 | 26 | 58 | 147 | 147 | 147 | 147 | CAMK | CAMK | 2424 | 2424 | 686 | 686 | 1 | 2058 | 2058 | 2058 | 2058 | 2058 | 419-458 | NA |
| W44186 m DRAX2 m | M | 34 | 55 | 28 | 55 | 28 | 55 | 148 | 148 | 148 | 148 | CAMK | CAMK | 2421 | 2421 | 809 | 809 | 1 | 2418 | 2418 | 2418 | 2418 | 2418 | x | NA |
| AA172300 h DRAX2 | H | 37 | 58 | 29 | 58 | 29 | 58 | 149 | 149 | 149 | 149 | CAMK | DAPK | 1628 | 1628 | 373 | 373 | 262 | 1380 | 1380 | 1380 | 1380 | 1380 | x | 23p1-23q2.3 |
| H01248 h DRAX1 h | H | 40 | 61 | 30 | 61 | 30 | 61 | 150 | 150 | 150 | 150 | CAMK | DAPK | 2671 | 2671 | 414 | 414 | 1 | 1242 | 1242 | 1242 | 1242 | 1242 | 91-110 | 7p11-q11 |
| AA021445 h | H | 45 | 68 | 31 | 68 | 31 | 68 | 151 | 151 | 151 | 151 | CAMK | DAPK | 1245 | 1245 | 414 | 414 | 1 | 1242 | 1242 | 1242 | 1242 | 1242 | x | 11q22.1-1q22.3 |
| 2R22.5-1 h | H | 43 | 64 | 32 | 64 | 32 | 64 | 152 | 152 | 152 | 152 | CAMK | ENK | 4321 | 4321 | 1311 | 1311 | 146 | 4078 | 4078 | 4078 | 4078 | 4078 | x | NA |
| R31237.1 h AAC33487 | H | 49 | 70 | 33 | 70 | 33 | 70 | 153 | 153 | 153 | 153 | CAMK | ENK | 2311 | 2311 | 436 | 436 | 871 | 2178 | 2178 | 2178 | 2178 | 2178 | 61-2281, 1258-12 | NA |
| W90839 m | M | 49 | 70 | 34 | 70 | 34 | 70 | 154 | 154 | 154 | 154 | CAMK | ENK | 2180 | 2180 | 729 | 729 | 1 | 2187 | 2187 | 2187 | 2187 | 2187 | x | NA |
| AA067665 h | H | 46 | 89 | 35 | 89 | 35 | 89 | 155 | 155 | 155 | 155 | CAMK | ENK | 1584 | 1584 | 520 | 520 | 1 | 1560 | 1560 | 1560 | 1560 | 1560 | x | NA |
| AA544638 m ODF88 m | M | 46 | 89 | 36 | 89 | 36 | 89 | 156 | 156 | 156 | 156 | CAMK | ENK | 1330 | 1330 | 1330 | 1330 | 77 | 4086 | 4086 | 4086 | 4086 | 4086 | x | 23p1-q37 |
| AA765735 h | H | 46 | 89 | 37 | 89 | 37 | 89 | 157 | 157 | 157 | 157 | CAMK | ENK | 1330 | 1330 | 1330 | 1330 | 77 | 4086 | 4086 | 4086 | 4086 | 4086 | x | NA |
| AA207220 h | H | 46 | 89 | 38 | 89 | 38 | 89 | 158 | 158 | 158 | 158 | CAMK | ENK | 5183 | 5183 | 926 | 926 | 155 | 2632 | 2632 | 2632 | 2632 | 2632 | 1002-1022 | NA |
| AA426580 h MAK V h | H | 47 | 88 | 39 | 88 | 39 | 88 | 159 | 159 | 159 | 159 | CAMK | ENK | 2391 | 2391 | 829 | 829 | 103 | 1999 | 1999 | 1999 | 1999 | 1999 | x | NA |
| Z36720 h | H | 50 | 71 | 40 | 71 | 40 | 71 | 160 | 160 | 160 | 160 | CAMK | ENK | 2145 | 2145 | 714 | 714 | 1 | 2142 | 2142 | 2142 | 2142 | 2142 | x | NA |
| SGK088 h | H | 39 | 73 | 41 | 73 | 41 | 73 | 161 | 161 | 161 | 161 | CAMK | MLCK | 2655 | 2655 | 874 | 874 | 1 | 2622 | 2622 | 2622 | 2622 | 2622 | x | NA |
| AA542015 m SGK088 m | M | 39 | 73 | 42 | 73 | 42 | 73 | 162 | 162 | 162 | 162 | CAMK | MLCK | 2655 | 2655 | 874 | 874 | 1 | 2622 | 2622 | 2622 | 2622 | 2622 | x | NA |
| AA19772 h | H | 52 | 74 | 43 | 74 | 43 | 74 | 163 | 163 | 163 | 163 | CAMK | Tro | 1251 | 1251 | 2268 | 2268 | 1 | 381 | 381 | 381 | 381 | 381 | x | NA |
| 5R72 B 2 h | H | 53 | 74 | 44 | 74 | 44 | 74 | 164 | 164 | 164 | 164 | CAMK | Tro | 3864 | 3864 | 1287 | 1287 | 1 | 3881 | 3881 | 3881 | 3881 | 3881 | x | 3q13.3-q21 |
| SGK309 h | H | 53 | 74 | 45 | 74 | 45 | 74 | 165 | 165 | 165 | 165 | CAMK | Unique | 2586 | 2586 | 514 | 514 | 406 | 1847 | 1847 | 1847 | 1847 | 1847 | x | 11p15.1-p15.2 |
| AA234451 h | H | 75 | 78 | 46 | 78 | 46 | 78 | 166 | 166 | 166 | 166 | CKI | CKI | 1620 | 1620 | 508 | 508 | 97 | 1620 | 1620 | 1620 | 1620 | 1620 | 843-892 | NA |
| AA435956 h | H | 82 | 80 | 47 | 80 | 47 | 80 | 167 | 167 | 167 | 167 | CKI | CKI | 2452 | 2452 | 478 | 478 | 406 | 1839 | 1839 | 1839 | 1839 | 1839 | x | NA |
| AA269859 h | H | 84 | 98 | 48 | 98 | 48 | 98 | 168 | 168 | 168 | 168 | CMGC | CDK | 1077 | 1077 | 269 | 269 | 2 | 742 | 742 | 742 | 742 | 742 | 84-119 | NA |
| AA09197 m | H | 81 | 95 | 49 | 95 | 49 | 95 | 169 | 169 | 169 | 169 | CMGC | CDK | 911 | 911 | 247 | 247 | 2 | 889 | 889 | 889 | 889 | 889 | x | NA |
| AA397553 h CRK7 | H | 85 | 99 | 50 | 99 | 50 | 99 | 170 | 170 | 170 | 170 | CMGC | CDK | 2813 | 2813 | 296 | 296 | 2 | 4470 | 4470 | 4470 | 4470 | 4470 | 1218-1238 | NA |
| AA1769239 h | H | 85 | 99 | 51 | 99 | 51 | 99 | 171 | 171 | 171 | 171 | CMGC | CDK | 4473 | 4473 | 1490 | 1490 | 6 | 1607 | 1607 | 1607 | 1607 | 1607 | 5623-6233 | NA |
| AA124976 m | M | x | x | 52 | x | 52 | x | 172 | 172 | 172 | 172 | CMGC | CDK | 1888 | 1888 | 534 | 534 | 1 | 1011 | 1011 | 1011 | 1011 | 1011 | x | NA |
| AA575655 m CORK m | M | x | x | 53 | x | 53 | x | 173 | 173 | 173 | 173 | CMGC | CDK | 1390 | 1390 | 211 | 211 | 1 | 633 | 633 | 633 | 633 | 633 | 163-181 | NA |
| AA319890 h CLK4 | H | 105 | 107 | 54 | 107 | 54 | 107 | 174 | 174 | 174 | 174 | CMGC | CLK | 2486 | 2486 | 499 | 499 | 1 | 1520 | 1520 | 1520 | 1520 | 1520 | x | NA |
| AA357536 h | H | 89 | 103 | 55 | 103 | 55 | 103 | 175 | 175 | 175 | 175 | CMGC | CLK | 1831 | 1831 | 545 | 545 | 34 | 1064 | 1064 | 1064 | 1064 | 1064 | 516-536 | NA |
| AA28608 h MOK | H | 90 | 104 | 56 | 104 | 56 | 104 | 176 | 176 | 176 | 176 | CMGC | RCK | 1859 | 1859 | 419 | 419 | 30 | 1257 | 1257 | 1257 | 1257 | 1257 | 14932 | NA |
| AB023153 h JCK | H | 91 | 104 | 57 | 104 | 57 | 104 | 177 | 177 | 177 | 177 | CMGC | RCK | 1859 | 1859 | 419 | 419 | 30 | 1257 | 1257 | 1257 | 1257 | 1257 | x | NA |
| AA939440 m | M | 165 | 201 | 58 | 201 | 58 | 201 | 178 | 178 | 178 | | | | | | | | | | | | | | | |

Table 1 (cont'd)

| Gene Name | SP | Priv Seq ID NA | Priv Seq ID AA | SEQ ID # na | SEQ ID # aa | Family | Group | Length NA | Length AA | ORF Start | ORF End | ORF Length | DNA Repeat | CHR location |
|-------------------------|----|----------------|----------------|-------------|-------------|--------|-----------|-----------|-----------|-----------|---------|------------|---------------|--------------------|
| BCO3 h | 1 | 148 | 184 | 58 | 184 | Other | C28C2 ce | 2164 | 538 | 113 | 1717 | 1608 | 246-267 | NA |
| AA711829 m | 1 | 148 | 184 | 58 | 184 | Other | C28C2 ce | 1568 | 378 | 1 | 1134 | 1134 | NA | NA |
| AA089102 h CAMKKB | 1 | 132 | 186 | 68 | 186 | Other | CAMKK | 1767 | 388 | 1 | 1764 | 1764 | 65-84 | 12q23-q14 |
| HF689 17 2 h | 1 | 158 | 194 | 67 | 194 | Other | CTRI | 3387 | 241 | 1850 | 2572 | 723 | 499-521 | NA |
| H5811 h | 1 | 134 | 170 | 68 | 189 | Other | DYRK | 3893 | 1171 | 183 | 3695 | 3513 | 1326-1348 | CHR7 |
| AA02183 h DYRK3 | 1 | 133 | 169 | 69 | 189 | Other | DYRK | 2141 | 553 | 253 | 1911 | 1659 | NA | NA |
| AA589241 m DYRK3 m | 1 | 133 | 169 | 70 | 190 | Other | DYRK | 741 | 188 | 3 | 506 | 504 | NA | NA |
| SR72 10 2 h R1927 h | 1 | 109 | 112 | 71 | 191 | Other | EPR | 5163 | 1849 | 20 | 4866 | 4947 | NA | NA |
| R43324 h HRI h R19509 h | 1 | 111 | 114 | 73 | 192 | Other | EPR | 1893 | 830 | 1 | 1890 | 1890 | NA | NA |
| 17000057519457 h | 1 | 135 | 171 | 74 | 193 | Other | Endop | 3055 | 253 | 219 | 977 | 759 | 2283-2365 | NA |
| AA013524 m | 1 | 135 | 171 | 75 | 194 | Other | Endop | 926 | 218 | 1 | 848 | 848 | NA | NA |
| 17000139801197 h IRAK1 | 1 | 137 | 173 | 76 | 195 | Other | IRAK | 1791 | 590 | 1 | 1788 | 1788 | NA | NA |
| AA840598 m IRAK1 m | 1 | 137 | 173 | 77 | 199 | Other | IRAK | 2243 | 362 | 1 | 1175 | 1176 | NA | NA |
| AA089547 h | 1 | 138 | 174 | 78 | 197 | Other | IRE | 2769 | 922 | 1 | 2768 | 2768 | NA | NA |
| HGP 6844466 | 1 | 139 | 175 | 79 | 198 | Other | KYK2 dd | 1857 | 322 | 179 | 1144 | 986 | NA | NA |
| AA449547 m | 1 | 115 | 116 | 81 | 200 | Other | KYK2 dd | 1251 | 280 | 2 | 841 | 840 | 602-621 | NA |
| SR57 10 2 m TESK2 m | 1 | 115 | 116 | 81 | 200 | Other | LINK | 140 | 41 | 2 | 124 | 123 | NA | NA |
| AA232253 h | 1 | 117 | 118 | 82 | 201 | Other | MLK | 2403 | 800 | 1 | 2400 | 2400 | NA | NA |
| A1375137 h | 1 | 209 | 210 | 83 | 202 | Other | MLK | 2509 | 835 | 1 | 2505 | 2505 | 2219-2238 | NA |
| H97685 h | 1 | 143 | 178 | 84 | 203 | Other | RIP | 2364 | 834 | 181 | 2092 | 1802 | NA | 10q31 |
| W20810 m | 1 | 144 | 180 | 85 | 204 | Other | RIP | 1073 | 289 | 3 | 689 | 687 | NA | NA |
| AA744236 h | 1 | 211 | 212 | 86 | 205 | Other | SCY1 sc | 2067 | 688 | 1 | 2064 | 2064 | NA | 1q23 |
| A052250 h | 1 | 225 | 228 | 87 | 208 | Other | SCY1 sc | 1739 | 505 | 174 | 1899 | 1515 | NA | NA |
| AA278842 h | 1 | 164 | 200 | 88 | 207 | Other | SCY1 sc | 2668 | 808 | 105 | 2528 | 2424 | 1764-1783 | 11q12-q13 Amplicon |
| AA599286 h | 1 | 145 | 181 | 89 | 208 | Other | SLOB7 | 1949 | 840 | 1 | 1949 | 1949 | NA | NA |
| AA459725 h | 1 | 146 | 182 | 90 | 209 | Other | SRPK | 1802 | 533 | 1 | 1599 | 1599 | NA | NA |
| SGK022 h | 1 | 149 | 185 | 91 | 210 | Other | STK22A | 1038 | 268 | 184 | 987 | 804 | NA | NA |
| AA080026 m SGK022 m | 1 | 149 | 185 | 92 | 211 | Other | STK22A | 1004 | 268 | 147 | 950 | 804 | NA | NA |
| AA399689 h | 1 | 150 | 186 | 93 | 212 | Other | STK22A | 1537 | 282 | 282 | 1244 | 876 | NA | 14p11-q11 |
| AA759539 h | 1 | 151 | 187 | 94 | 213 | Other | STK22A | 1322 | 358 | 101 | 1174 | 1074 | NA | NA |
| AA483975 h | 1 | 153 | 189 | 95 | 214 | Other | TSK | 822 | 273 | 1 | 819 | 819 | NA | NA |
| AA905446 h | 1 | 223 | 224 | 96 | 215 | Other | TSK | 1099 | 216 | 365 | 1012 | 849 | NA | NA |
| H29974 h | 1 | 69 | 102 | 97 | 216 | Other | UNC | 1836 | 333 | 2 | 1000 | 999 | NA | NA |
| AA48804 m H29974 m | 1 | 69 | 102 | 97 | 216 | Other | UNC | 1490 | 412 | 1 | 1236 | 1236 | 701-729 | NA |
| AA215311 h | 1 | 155 | 191 | 98 | 217 | Other | UNC | 2011 | 341 | 189 | 1221 | 1023 | NA | NA |
| AA018191 h | 1 | 154 | 190 | 100 | 219 | Other | UNC | 2759 | 481 | 113 | 1555 | 1443 | NA | 15q23 |
| AA311714 h | 1 | 155 | 192 | 101 | 220 | Other | UNC | 1876 | 565 | 135 | 1833 | 1695 | NA | NA |
| SGK384 h | 1 | 106 | 108 | 102 | 221 | Other | Unique | 117 | 39 | 1 | 117 | 117 | NA | NA |
| AA210451 m SGK384 m | 1 | 106 | 108 | 103 | 222 | Other | Unique | 2121 | 349 | 222 | 1268 | 1047 | 2251-2286 | NA |
| SGK071 2 h | 1 | 161 | 197 | 104 | 223 | Other | Unique | 2115 | 704 | 1 | 2112 | 2112 | 5776, 518-537 | NA |
| AA118352 m SGK071 m | 1 | 161 | 197 | 105 | 224 | Other | Unique | 1729 | 840 | 3 | 1822 | 1820 | NA | NA |
| 0.8853.9 h | 1 | 162 | 198 | 106 | 225 | Other | Unique | 2461 | 540 | 1 | 1820 | 1820 | 240-259 | NA |
| AA396801 m | 1 | 163 | 199 | 107 | 226 | Other | Unique | 1886 | 365 | 3 | 1097 | 1095 | NA | NA |
| AA871275 h VRK3 | 1 | 163 | 199 | 108 | 227 | Other | VRK | 1425 | 474 | 1 | 1422 | 1422 | 18q13 | NA |
| ST1575 m VRK3 m | 1 | 163 | 199 | 109 | 228 | Other | VRK | 1009 | 234 | 3 | 704 | 702 | 937-957 | NA |
| AA42647 h MPSK1 | 1 | 138 | 172 | 110 | 229 | Other | YPL238 sc | 918 | 305 | 1 | 815 | 815 | NA | 3cen-3021 |
| H05721 h | 1 | 168 | 202 | 111 | 230 | Other | YOS9 ce | 2668 | 581 | 95 | 1837 | 1743 | NA | 1022-3.31 Amplicon |
| A086885 h | 1 | 88 | 100 | 112 | 231 | Other | NEK | 2463 | 898 | 7 | 2100 | 2094 | NA | NA |
| AA838348 h | 1 | 120 | 124 | 113 | 232 | Other | NEK | 2511 | 838 | 1 | 2508 | 2508 | NA | NA |
| R66668 h MKK8 | 1 | 121 | 125 | 114 | 233 | Other | STE11 | 3036 | 1011 | 1 | 3033 | 3033 | NA | 1p32.3-p31.1 |
| PAK6 h 5895-20-11 | 1 | 219 | 220 | 115 | 234 | Other | STE20-02 | 2160 | 719 | 1 | 2157 | 2157 | NA | 20q12 |
| SR1K106 h 2841-9-4 h | 1 | 128,127 | 129,130 | 116 | 235 | Other | TK | 2460 | 495 | 1 | 1485 | 1485 | NA | 12p12.3 |
| AA086024 m | 1 | 128,127 | 130 | 117 | 236 | Other | TK | 1793 | 183 | 1 | 549 | 549 | 1382-1392 | NA |
| SGK2alpha h | 1 | 87 | 101 | 118 | 237 | Other | AGC | 1812 | 387 | 88 | 1188 | 1101 | NA | NA |
| H08850 h CCRK | 1 | 87 | 101 | 120 | 238 | Other | COK | 1359 | 452 | 1 | 1356 | 1356 | NA | 9q21.1-q21.3 |
| NM 007170 h TESK2 | 1 | 1 | 1 | 121 | 239 | Other | LINK | 3016 | 555 | 398 | 2090 | 1665 | NA | NA |

Table 2

| SP | ID# | na | ID# | aa | Patent | Seq | Family | Group | Pecore | Length | ID | match | % | Identity | % | Similar | nraa | Match | Description | Kinase Domain(s) start | Kinase Domain(s) end | Profile start | Profile end |
|----|-----|-----|-----|-----|-----------|-----|--------|-------|--------|--------|-----|-------|-----|----------|-----|---------|-------------|--|-------------|------------------------|----------------------|---------------|-------------|
| H | 1 | 122 | AGC | GRK | 2.7e-314 | 688 | 887 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | CAB45657.1 | BAR22 [Homo sapiens] | 191 | 453 | 1 | 261 | |
| M | 2 | 123 | AGC | GRK | 1.30E-190 | 378 | 371 | 98 | 89 | 89 | 89 | 89 | 89 | 89 | 89 | 89 | NP_037029.1 | Adreneglor receptor kinase, beta 2 [G-protein-linked receptor kin | 3 | 143 | 121 | 261 | |
| H | 3 | 124 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | CAB76471.1 | Serine/threonine protein kinase [Homo sapiens] | 26 | 266 | 1 | 261 | |
| H | 4 | 125 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | CAB76471.1 | Serine/threonine protein kinase [Homo sapiens] | 23 | 283 | 1 | 261 | |
| H | 5 | 126 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_037386.1 | TANK-binding kinase 1 [Homo sapiens] | 9 | 304 | 1 | 261 | |
| H | 6 | 127 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_037386.1 | TANK-binding kinase 1 [Homo sapiens] | 35 | 310 | 1 | 261 | |
| M | 7 | 128 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | BAA76817.1 | KIAA0973 protein [Homo sapiens] | 24 | 44 | 242 | 261 | |
| M | 8 | 129 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AAF55594.1 | CG7718 gene product [Drosophila melanogaster] | 90 | 363 | 1 | 261 | |
| H | 9 | 130 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | BAAT76809.1 | KIAA0963 protein [Homo sapiens] | 651 | 907 | 1 | 261 | |
| H | 10 | 131 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_002733.1 | Protein kinase C, mu [Homo sapiens] | 19 | 24 | 256 | 261 | |
| H | 11 | 132 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | P05127 | Protein kinase C, BETA-II TYPE (PKC-BETA-2) [Homo sapiens] | 576 | 832 | 1 | 261 | |
| H | 12 | 133 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_05804.1 | Protein kinase C, nu [Homo sapiens] | 559 | 818 | 1 | 261 | |
| M | 13 | 134 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_037487.1 | PKNbeta [Homo sapiens] | 1 | 134 | 126 | 261 | |
| H | 14 | 135 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | JC7083 | Protein kinase N beta [Homo sapiens] | 81 | 333 | 1 | 261 | |
| H | 15 | 136 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AA02495.1 | Ribosomal protein S6 kinase 3 [Homo sapiens] | 225 | 459 | 1 | 261 | |
| H | 16 | 137 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_036556.1 | Ribosomal protein S6 kinase, 52kD, polypeptide 1 [Homo sapien | 73 & 428 | 330 & 683 | 1 | 261 | |
| H | 17 | 138 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_055311.1 | Ribosomal protein S6 kinase, 90kD, polypeptide 6 [Homo sapien | 153 | 539 | 1 | 261 | |
| H | 18 | 139 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AA030182.1 | Unknown [Homo sapiens] | 98 | 355 | 1 | 261 | |
| M | 19 | 140 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AD041091.1 | SGK [Homo sapiens] | 98 | 355 | 1 | 261 | |
| M | 20 | 141 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_035491.1 | Serum/glucocorticoid regulated kinase [Mus musculus] | 1 | 169 | 24 | 261 | |
| H | 21 | 142 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AAF12757.2 | Protein kinase [Homo sapiens] | 162 | 389 | 1 | 261 | |
| H | 22 | 143 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_009215.1 | Protein tyrosine kinase 9-like (A6-related protein) [Homo sapiens] | 10 | 17 | 253 | 261 | |
| H | 23 | 144 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AAF27051.1 | SGK-like protein SGK [Homo sapiens] | 40 | 333 | 1 | 261 | |
| H | 24 | 145 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | CA0404119.1 | Phosphoprotein [Homo sapiens] | 368 | 625 | 1 | 261 | |
| M | 25 | 146 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | O15075 | DCAMKL1 [DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1] | 59 | 297 | 1 | 261 | |
| M | 26 | 147 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AAF26675.1 | CPG16 [Mus musculus] | 415 | 673 | 1 | 261 | |
| M | 27 | 148 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | O15075 | DCAMKL1 [DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1] | 514 | 771 | 1 | 261 | |
| M | 28 | 149 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AAF26675.1 | CPG16 [Mus musculus] | 33 | 293 | 1 | 261 | |
| M | 29 | 150 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_004217.1 | Death-associated protein kinase-related 2 | 32 | 293 | 1 | 261 | |
| M | 30 | 151 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_004217.1 | Death-associated protein kinase-related 2 | 61 | 321 | 1 | 261 | |
| H | 31 | 152 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_004751.1 | Death-associated protein kinase-related 1 | 8 | 259 | 1 | 261 | |
| H | 32 | 153 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | BAAT76843.1 | Hypothetical protein F49C5.4 - [Caenorhabditis elegans] | 74 | 325 | 1 | 261 | |
| H | 33 | 154 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | T22427 | Hypothetical protein F49C5.4 - [Caenorhabditis elegans] | 56 | 307 | 1 | 261 | |
| H | 34 | 155 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AA015093.1 | Cdc25C associated protein kinase C-TAK1 [Homo sapiens] | 59 | 340 | 1 | 261 | |
| H | 35 | 156 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AA015093.1 | Cdc25C associated protein kinase C-TAK1 [Homo sapiens] | 999 | 1258 | 1 | 261 | |
| M | 36 | 157 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | BA09484.1 | R31237.1, partial CDS [Homo sapiens] | 1 | 156 | 23 | 261 | |
| M | 37 | 158 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | BA09484.1 | KIAA0135 gene, related to p1m-1 oncogene, [Homo sapiens] | 20 | 271 | 1 | 261 | |
| H | 38 | 159 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | BA09484.1 | KIAA0781 protein [Homo sapiens] | 53 | 304 | 1 | 261 | |
| H | 39 | 160 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_056555.1 | KIAA0537 gene product [Homo sapiens] | 61 | 320 | 1 | 261 | |
| H | 40 | 161 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_055401.1 | Homomally upregulated neu tumor-associated kinase [Homo sa | 570 | 825 | 1 | 261 | |
| H | 41 | 162 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AAAT73168.1 | Skeletal muscle myosin light chain kinase [Gallus gallus] | 620 & 1066 | 873 & 1356 | 1 | 261 | |
| M | 42 | 163 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | BA02535.1 | KIAA1297 protein [Homo sapiens] | 3 | 78 | 186 | 261 | |
| M | 43 | 164 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | BA02535.1 | KIAA1297 protein [Homo sapiens] | 985 | 1239 | 1 | 261 | |
| H | 44 | 165 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_006995.1 | STK with Dbl- and pleckstrin homology domains [Homo sapiens] | 116 | 381 | 1 | 261 | |
| H | 45 | 166 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | P25323 | MLCK [Dictyostelium discoideum] | 34 | 313 | 1 | 261 | |
| H | 46 | 167 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AAF59340.1 | CG11533 gene product [Drosophila melanogaster] | 21 | 471 | 1 | 261 | |
| H | 47 | 168 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | AAF59340.1 | CG11533 gene product [Drosophila melanogaster] | 21 | 471 | 1 | 261 | |
| H | 48 | 169 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_038527.1 | PFTARE protein kinase, 1 [Homo sapiens] | 1 | 191 | 23 | 261 | |
| H | 49 | 170 | AGC | GRK | 5.80E-106 | 419 | 282 | 71 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | NP_004187.1 | Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa | 1 | 191 | 23 | 261 | |

Table 2 (cont'd)

| | | | | | | | | | | | | | | | |
|---|-----|-----|--------------|----------|-----------|------|------|-----|-----|-------------|---|-----|------|-----|-----|
| M | 50 | 170 | CMGC | CDK | 2.90E-64 | 296 | 193 | 65 | 78 | NP_004187.1 | Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens] | 1 | 240 | 24 | 261 |
| H | 51 | 171 | CMGC | CDK | 1.10E-264 | 1490 | 1490 | 100 | 100 | AAF38401.1 | CDC2-related protein kinase 7 [Homo sapiens] | 21 | 1020 | 1 | 261 |
| H | 52 | 172 | CMGC | CDK | 9.20E-101 | 534 | 377 | 82 | 82 | AAF38509.1 | NKIAMRE [Homo sapiens] | 4 | 385 | 1 | 261 |
| M | 53 | 173 | CMGC | CDK | 1.40E-128 | 337 | 225 | 92 | 96 | AAF34871.1 | NKIATRE alpha [Rattus norvegicus] | 1 | 28 | 235 | 261 |
| M | 54 | 174 | CMGC | CDK | 3.00E-68 | 211 | 159 | 79 | 84 | NP_038251.1 | Cell cycle related kinase [Homo sapiens] | 1 | 153 | 134 | 261 |
| H | 55 | 175 | CMGC | CLK | 1.50E-242 | 499 | 436 | 91 | 93 | NP_031740.1 | Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens] | 177 | 493 | 1 | 261 |
| H | 56 | 176 | CMGC | RCK | 9.10E-89 | 544 | 343 | 57 | 64 | AAD12179.1 | Extracellular signal-regulated kinase 7, ERK7 [Rattus norvegicus] | 13 | 305 | 1 | 261 |
| H | 57 | 177 | CMGC | RCK | 2.30E-189 | 419 | 419 | 100 | 100 | NP_055041.1 | Renal tumor antigen [Homo sapiens] | 4 | 285 | 1 | 261 |
| H | 58 | 178 | CMGC | RCK | 1.50E-180 | 632 | 632 | 100 | 100 | AAF37278.1 | Intestinal cell kinase [Homo sapiens] | 4 | 284 | 1 | 261 |
| M | 59 | 179 | CMGC | RCK | 1.60E-79 | 413 | 198 | 60 | 77 | P20689 | MLCK [Rattus norvegicus] | 109 | 364 | 1 | 261 |
| H | 60 | 180 | Microbial PK | GR262 sc | 2.50E-45 | 253 | 102 | 46 | 67 | AAF50799.1 | CG10673 gene product [Drosophila melanogaster] | 101 | 187 | 65 | 147 |
| H | 61 | 181 | Other | C26C2 ce | 2.30E-158 | 509 | 258 | 100 | 100 | CAB70864.1 | Hypothetical protein [Homo sapiens] | 2 | 287 | 1 | 261 |
| M | 62 | 182 | Other | C26C2 ce | 1.80E-152 | 281 | 243 | 94 | 98 | CAB70864.1 | Hypothetical protein [Homo sapiens] | 59 | 86 | 235 | 261 |
| M | 63 | 183 | Other | C26C2 ce | 6.70E-300 | 1952 | 1193 | 99 | 99 | NP_055638.1 | KIAA0344 gene product [Homo sapiens] | 221 | 479 | 1 | 261 |
| H | 64 | 184 | Other | C26C2 ce | 1.10E-254 | 535 | 535 | 100 | 100 | NP_037524.1 | Nuclear receptor binding protein [Homo sapiens] | 73 | 327 | 1 | 261 |
| M | 65 | 185 | Other | C26C2 ce | 2.50E-208 | 378 | 372 | 98 | 100 | NP_037524.1 | Nuclear receptor binding protein [Homo sapiens] | 1 | 170 | 85 | 261 |
| H | 66 | 186 | Other | CAMKK | 3.80E-148 | 588 | 588 | 100 | 100 | AAD31507.1 | Ca2+/calmodulin-dependent protein kinase beta [Homo sapiens] | 165 | 446 | 1 | 261 |
| H | 67 | 187 | Other | CTR1 | 9.90E-24 | 287 | 87 | 33 | 52 | QJ1743 | Hypothetical 33.8K protein - rabbit fibroma virus | 24 | 285 | 1 | 261 |
| H | 68 | 188 | Other | DYRK | 0 | 1171 | 1137 | 97 | 99 | AAD52566.1 | Nuclear body associated kinase 1a [Mus musculus] | 199 | 527 | 1 | 261 |
| H | 69 | 189 | Other | DYRK | 2.10E-280 | 553 | 553 | 100 | 100 | NP_003573.1 | Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 | 174 | 487 | 1 | 261 |
| M | 70 | 190 | Other | DYRK | 2.30E-95 | 168 | 149 | 90 | 96 | NP_003573.1 | Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 | 76 | 103 | 235 | 261 |
| H | 71 | 191 | Other | EIFK | 0 | 1649 | 1493 | 90 | 96 | NP_038747.1 | GCN2 eIF2alpha kinase [Mus musculus] | 167 | 583 | 1 | 261 |
| H | 73 | 192 | Other | EIFK | 1.50E-220 | 630 | 630 | 100 | 100 | NP_055228.1 | Heme-regulated initiation factor 2-alpha kinase [Homo sapiens] | 101 | 187 | 65 | 147 |
| M | 74 | 193 | Other | Endop | 2.50E-45 | 253 | 102 | 45 | 67 | AAF50799.1 | CG10673 gene product [Drosophila melanogaster] | 116 | 150 | 116 | 147 |
| M | 75 | 194 | Other | Endop | 3.70E-45 | 216 | 100 | 45 | 64 | AAF50799.1 | (AE003587) CG10673 gene product [Drosophila melanogaster] | 165 | 443 | 1 | 261 |
| H | 76 | 195 | Other | IRAK | 0 | 596 | 596 | 100 | 100 | NP_009130.1 | Interleukin-1 receptor-associated kinase M [Homo sapiens] | 1 | 239 | 19 | 261 |
| M | 77 | 196 | Other | IRAK | 1.20E-170 | 392 | 293 | 75 | 85 | NP_009130.1 | Interleukin-1 receptor-associated kinase M [Homo sapiens] | 516 | 777 | 1 | 261 |
| H | 78 | 197 | Other | IRE | 1.5e-323 | 922 | 746 | 82 | 89 | NP_036146.1 | Irf1, inositol-requiring 1 gene [Mus musculus] | 32 | 318 | 1 | 261 |
| H | 79 | 198 | Other | KYK2 dd | 8.70E-40 | 225 | 102 | 45 | 82 | AAF48758.1 | CG1173 gene product [Drosophila melanogaster] | 12 | 266 | 1 | 261 |
| M | 80 | 199 | Other | KYK2 dd | 5.90E-32 | 280 | 109 | 32 | 50 | AAF48758.1 | CG1173 gene product [Drosophila melanogaster] | 12 | 266 | 1 | 261 |
| M | 81 | 200 | Other | LMK | 2.60E-17 | 41 | 37 | 92 | 95 | NP_009101.1 | leish-specific kinase 2 [Homo sapiens] | 18 | 259 | 1 | 261 |
| H | 82 | 201 | Other | MLK | 2.50E-282 | 800 | 799 | 100 | 100 | AAF63490.1 | Mixed lineage kinase [Homo sapiens] | 483 | 723 | 1 | 261 |
| H | 83 | 202 | Other | MLK | 8.60E-251 | 835 | 835 | 100 | 100 | AAD29632.1 | Puative protein-tyrosine kinase [Homo sapiens] | 357 | 620 | 1 | 261 |
| H | 84 | 203 | Other | RIP | 2.20E-158 | 634 | 365 | 100 | 100 | BAA32317.1 | KIAA0472 protein [Homo sapiens] | 7 | 27 | 181 | 202 |
| M | 85 | 204 | Other | RIP | 5.30E-158 | 289 | 288 | 100 | 100 | AAF03133.1 | Receptor interacting protein 3 [Mus musculus] | 57 | 83 | 50 | 78 |
| H | 86 | 205 | Other | SCY1 sc | 0 | 688 | 688 | 100 | 100 | CAB55300.1 | Hypothetical protein [Homo sapiens] | 32 | 327 | 1 | 261 |
| H | 87 | 206 | Other | SCY1 sc | 1.70E-209 | 505 | 354 | 98 | 98 | BAA92598.1 | KIAA1360 protein [Homo sapiens] | 65 | 131 | 47 | 116 |
| H | 88 | 207 | Other | SCY1 sc | 2.20E-157 | 808 | 396 | 45 | 61 | AAF56933.1 | CG1973 gene product [Drosophila melanogaster] | 230 | 305 | 81 | 143 |
| H | 89 | 208 | Other | SLOB? | 7.40E-196 | 649 | 649 | 100 | 100 | BAA91097.1 | Unamed protein product [Homo sapiens] | 79 | 531 | 1 | 261 |
| H | 90 | 209 | Other | SRPK | 5.80E-252 | 533 | 533 | 100 | 100 | NP_055185.1 | Serine/threonine kinase 23 [Homo sapiens] | 10 | 265 | 1 | 261 |
| H | 91 | 210 | Other | STK22A | 3.80E-53 | 268 | 122 | 46 | 70 | NP_033461.1 | Serine/threonine kinase 22A (spERMogenesis associated) [Mus musculus] | 25 | 280 | 1 | 261 |
| M | 92 | 211 | Other | STK22 | 2.70E-52 | 268 | 127 | 48 | 68 | NP_033462.1 | Serine/threonine kinase 22B (spERMogenesis associated) [Mus musculus] | 12 | 272 | 1 | 261 |
| H | 93 | 212 | Other | STK22A | 4.60E-16 | 292 | 112 | 45 | 64 | NP_033461.1 | Serine/threonine kinase 22A (spERMogenesis associated) [Mus musculus] | 12 | 272 | 1 | 261 |
| H | 94 | 213 | Other | TSK | 5.10E-123 | 358 | 322 | 90 | 96 | NP_033462.1 | Serine/threonine kinase 22B (spERMogenesis associated) [Mus musculus] | 12 | 267 | 1 | 261 |
| H | 95 | 214 | Other | TSK | 2.10E-33 | 273 | 122 | 46 | 62 | NP_033461.1 | Serine/threonine kinase 22B (spERMogenesis associated) [Mus musculus] | 1 | 213 | 7 | 261 |
| H | 96 | 215 | Other | TSK | 2.50E-32 | 216 | 93 | 41 | 58 | NP_033462.1 | Serine/threonine kinase 22B (spERMogenesis associated) [Mus musculus] | 1 | 329 | 1 | 261 |
| H | 97 | 216 | Other | UNC | 0.000062 | 333 | 57 | 36 | 56 | AAD32787.1 | Puative protein kinase [Arabidopsis thaliana] | 80 | 408 | 1 | 261 |
| M | 98 | 217 | Other | UNC | 0.002492 | 412 | 53 | 37 | 52 | BAA77341.1 | UNC-51-like kinase (ULK) 2 [Mus musculus] | 8 | 340 | 1 | 261 |
| H | 99 | 218 | Other | UNC | 0.001096 | 341 | 50 | 36 | 56 | BAA77341.1 | UNC-51-like kinase (ULK) 2 [Mus musculus] | 57 | 313 | 1 | 261 |
| H | 100 | 219 | Other | UNC | 1.90E-68 | 480 | 247 | 100 | 100 | T17265 | Hypothetical protein DkFp434C131.1 - human (fragment) | 4 | 265 | 1 | 261 |
| H | 101 | 220 | Other | UNC | 1.60E-208 | 565 | 468 | 96 | 96 | BAA91270.1 | Unamed protein product [Homo sapiens] | 4 | 265 | 1 | 261 |
| H | 102 | 221 | Other | Unique | 6.70E-10 | 39 | 27 | 69 | 90 | AAD00575.1 | Serum-inducible kinase [Homo sapiens] | 1 | 39 | 84 | 124 |

Table 2 (cont'd)

| | | | | | | | | | | | | | | |
|-------|-----|-------|-----------|-----------|------|------|-----|-----|-------------|---|-----|-----|-----|-----|
| M 103 | 222 | Other | Unique | 0.00022 | 349 | 38 | 30 | 50 | CAA18116.1 | Serine/threonine protein kinase like protein [Arabidopsis thaliana] | 80 | 159 | 1 | 88 |
| H 104 | 223 | Other | Unique | 0.000126 | 704 | 54 | 30 | 45 | BAA88578.1 | KIAA1284 protein [Homo sapiens] | 1 | 246 | 25 | 261 |
| M 105 | 224 | Other | Unique | 0.007365 | 540 | 25 | 42 | 61 | AAF47916.1 | Tie gene product [Drosophila melanogaster] | 9 | 104 | 168 | 261 |
| H 106 | 225 | Other | Unique | 0.31334 | 540 | 52 | 30 | 42 | P10162 | SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo sapiens] | 1 | 272 | 18 | 73 |
| M 107 | 226 | Other | Unique | 0.022948 | 365 | 25 | 34 | 57 | NP_006276.1 | testis-specific kinase 1 [Homo sapiens] | 68 | 96 | 42 | 71 |
| H 108 | 227 | Other | VRK | 3.10E-263 | 474 | 474 | 100 | 100 | BAA90769.1 | Vaccinia related kinase 3 [Homo sapiens] | 247 | 318 | 63 | 136 |
| M 109 | 228 | Other | VRK | 1.20E-111 | 234 | 191 | 82 | 90 | BAA90769.1 | Vaccinia related kinase 3 [Homo sapiens] | 7 | 78 | 63 | 136 |
| H 110 | 229 | Other | YPL236.sc | 7.40E-144 | 305 | 304 | 100 | 100 | AAC28337.1 | MPSK [Homo sapiens] | 20 | 290 | 1 | 261 |
| H 111 | 230 | Other | YQ09.ce | 5.10E-49 | 581 | 135 | 43 | 63 | AAF46188.1 | CG4523 gene product [Drosophila melanogaster] | 156 | 507 | 1 | 261 |
| H 112 | 231 | STE | NEK | 3.30E-30 | 698 | 122 | 48 | 67 | P51954 | NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus] | 4 | 251 | 1 | 261 |
| H 113 | 232 | STE | NEK | 2.70E-119 | 836 | 357 | 86 | 86 | AAD31938.1 | [AC007055] unknown [Homo sapiens] | 52 | 308 | 1 | 261 |
| H 114 | 233 | STE | STE11 | 1.10E-291 | 1011 | 1011 | 100 | 100 | NP_004663.1 | mitogen-activated protein kinase kinase kinase 6 [Homo sapiens] | 376 | 629 | 6 | 261 |
| H 115 | 234 | STE | STE20-02 | 7.70E-177 | 719 | 719 | 100 | 100 | BAA94194.1 | (AB040812) protein kinase PAK5 [Homo sapiens] | 449 | 700 | 1 | 261 |
| H 116 | 235 | TK | RTK-20 | 4.90E-24 | 485 | 77 | 38 | 56 | AA088465.1 | (U40827) protein tyrosine kinase [Mus musculus] | 187 | 453 | 1 | 261 |
| M 117 | 236 | TK | RTK-20 | 5.30E-18 | 183 | 53 | 39 | 57 | NP_032036.1 | fibroblast growth factor receptor 3 [Mus musculus] | 8 | 143 | 123 | 261 |
| H 118 | 237 | AGC | SGK | 6.30E-112 | 367 | 367 | 100 | 100 | AAF12757.2 | SGK2alpha protein kinase [Homo sapiens] | 35 | 292 | 1 | 261 |
| H 120 | 238 | CMGC | CDK | 2.80E-137 | 452 | 452 | 100 | 100 | NP_036251.1 | Cell cycle related kinase [Homo sapiens] | 4 | 267 | 1 | 261 |
| H 121 | 239 | Other | LIMK | 6.50E-233 | 555 | 555 | 100 | 100 | NP_009101.1 | Testis-specific kinase 2 [Homo sapiens] | 62 | 293 | 5 | 261 |

164
Table 3

| Tissue | Tumor - sym | Normal - sym | Tumor - to | Tumor cells | Normal | Endos | p33 | SEQ 003 | ANED 5 | TBX | SEQ 006 | ANED 6 | ANED 7 | CASED 8 | SEQ 11 | EP | SEQ 12 | PK | SEQ 14 | H1K | SEQ 16 | RS |
|---------------------------|-------------|--------------|------------|-------------|--------|-------|-----|---------|--------|---------|---------|--------|--------|---------|--------|----|--------|----|--------|-----|--------|----|
| adrenal gland - h | | | | | | | | 7480 | 13811 | 583727 | 29845 | 347051 | 56988 | 11609 | | | | | | | | |
| lymph node - h | 2 | | | | | | | 8151 | 32265 | 1202494 | 118257 | 105118 | 55339 | 19921 | | | | | | | | |
| bone marrow - h | 3 | | | | | | | 4465 | 9236 | 1477566 | 35367 | 322371 | 33850 | 13151 | | | | | | | | |
| mammary gland - h | 4 | | | | | | | 964 | 316 | 109887 | 4031 | 4318 | 1084 | 1993 | | | | | | | | |
| testis - h | 5 | | | | | | | 9689 | 5273 | 229703 | 54022 | 21862 | 7801 | 774 | | | | | | | | |
| pancreas - h | 6 | | | | | | | 5433 | 3574 | 334665 | 50925 | 32290 | 851 | 11829 | | | | | | | | |
| carotid - h | 7 | | | | | | | 6350 | 19704 | 767233 | 84606 | 35857 | 16370 | 29263 | | | | | | | | |
| pituitary gland - h | 8 | | | | | | | 9542 | 7686 | 712184 | 80497 | 38563 | 19473 | 11010 | | | | | | | | |
| testis - h | 9 | | | | | | | 13719 | 6045 | 967041 | 95491 | 20150 | 23443 | 13781 | | | | | | | | |
| placenta - h | 10 | | | | | | | 6763 | 15456 | 1232178 | 46306 | 45070 | 24271 | 13067 | | | | | | | | |
| testis - h | 11 | | | | | | | 4707 | 10839 | 537527 | 51063 | 67946 | 31171 | 19988 | | | | | | | | |
| prostate - h | 12 | | | | | | | 3477 | 1784 | 122058 | 60267 | 49912 | 11799 | 9464 | | | | | | | | |
| testis - h | 13 | | | | | | | 3307 | 5294 | 1348111 | 26106 | 35129 | 17029 | 10418 | | | | | | | | |
| salivary gl. - h | 14 | | | | | | | 2725 | 3698 | 428781 | 37947 | 37758 | 11433 | 13806 | | | | | | | | |
| testis - h | 15 | | | | | | | 6315 | 6461 | 1305487 | 79678 | 56484 | 31011 | 34594 | | | | | | | | |
| skeletal muscle - h | 16 | | | | | | | 5483 | 3765 | 187692 | 81053 | 12319 | 10685 | 11874 | | | | | | | | |
| heart - h | 17 | | | | | | | 3012 | 1915 | 227834 | 21479 | 20873 | 6357 | 11717 | | | | | | | | |
| small intestine - h | 18 | | | | | | | 3020 | 5561 | 535116 | 28567 | 28593 | 11120 | 12229 | | | | | | | | |
| kidney - h | 19 | | | | | | | 3588 | 5453 | 412001 | 41491 | 24102 | 7829 | 8496 | | | | | | | | |
| spinal cord - h | 20 | | | | | | | 3186 | 2798 | 224006 | 21586 | 12872 | 12294 | 4644 | | | | | | | | |
| testis - h | 21 | | | | | | | 3163 | 4478 | 338587 | 34563 | 16261 | 11556 | 8365 | | | | | | | | |
| spleen - h | 22 | | | | | | | 3364 | 1518 | 206605 | 46111 | 29975 | 10799 | 8189 | | | | | | | | |
| lung - h | 23 | | | | | | | 4121 | 1921 | 488627 | 25513 | 25347 | 10630 | 4418 | | | | | | | | |
| stomach - h | 24 | | | | | | | 2858 | 419 | 312882 | 33861 | 12206 | 5870 | 3999 | | | | | | | | |
| testis - h | 25 | | | | | | | 6342 | 15392 | 1250953 | 99041 | 19148 | 117943 | 9666 | | | | | | | | |
| thyroid - h | 26 | | | | | | | 7656 | 4996 | 1874063 | 129888 | 83645 | 46507 | 31130 | | | | | | | | |
| HPAEC | 28 | | | | | | | 7304 | 0 | 58668 | 34171 | 26274 | 3919 | 14479 | | | | | | | | |
| thyroid gland - h | 29 | | | | | | | 3700 | 1073 | 194311 | 42836 | 25961 | 9827 | 9143 | | | | | | | | |
| RPTEC | 30 | | | | | | | 24571 | 1927 | 80360 | 21213 | 3357 | 3397 | 15054 | | | | | | | | |
| testis - h | 31 | | | | | | | 6724 | 3097 | 40944 | 40944 | 4981 | 15260 | 16042 | | | | | | | | |
| HMEC | 32 | | | | | | | 7791 | 1355 | 138666 | 24427 | 15301 | 4715 | 17137 | | | | | | | | |
| uterus - h | 33 | | | | | | | 5386 | 4649 | 534257 | 34433 | 33931 | 14725 | 15085 | | | | | | | | |
| HCAEC | 34 | | | | | | | 7676 | 0 | 62247 | 26246 | 12123 | 1768 | 28455 | | | | | | | | |
| pancreas - h | 35 | | | | | | | 11088 | 515 | 15818 | 15818 | 14140 | 8511 | 46437 | | | | | | | | |
| lymph node - h | 36 | | | | | | | 6132 | 731 | 47839 | 15791 | 20735 | 8420 | 2812 | | | | | | | | |
| Skeletal muscle - h | 37 | | | | | | | 5906 | 77 | 0 | 11060 | 5411 | 5264 | 2070 | | | | | | | | |
| testis - h | 38 | | | | | | | 8689 | 2171 | 144493 | 18355 | 15506 | 5458 | 2447 | | | | | | | | |
| heart - h | 39 | | | | | | | 7091 | 245 | 15301 | 15301 | 9651 | 3825 | 3825 | | | | | | | | |
| thyroid - h | 40 | | | | | | | 9710 | 2472 | 87220 | 40613 | 17473 | 10164 | 15027 | | | | | | | | |
| Duodenum - h | 41 | | | | | | | 2879 | 0 | 28026 | 9776 | 14899 | 4049 | 9070 | | | | | | | | |
| testis - h | 42 | | | | | | | 12395 | 3365 | 21478 | 20505 | 18311 | 15818 | 3363 | | | | | | | | |
| Salivary gl. - h | 43 | | | | | | | 4496 | 1734 | 12171 | 1734 | 4150 | 12171 | 3293 | | | | | | | | |
| testis - h | 44 | | | | | | | 6962 | 23669 | 33514 | 19562 | 14856 | 17332 | 4385 | | | | | | | | |
| HT 218-normal | | | | | | | | 115 | 357 | 9191 | 3368 | 2191 | 1738 | 134 | | | | | | | | |
| HT 213-normal | | | | | | | | 363 | 0 | 427 | 9712 | 1918 | 0 | 144 | | | | | | | | |
| HT 157-normal | | | | | | | | 0 | 17 | 26470 | 12730 | 125 | 12730 | 654 | | | | | | | | |
| Bov-13 | | | | | | | | 356 | 356 | 563114 | 49109 | 10630 | 20146 | 46927 | | | | | | | | |
| Bov-12 | | | | | | | | 354 | 354 | 58750 | 69954 | 9439 | 12012 | 3467 | | | | | | | | |
| carotid - h | | | | | | | | 344 | 0 | 242 | 21691 | 2939 | 1748 | 3951 | | | | | | | | |
| testis - h | | | | | | | | 342 | 0 | 565 | 2034 | 2890 | 0 | 2454 | | | | | | | | |
| RPTEC | | | | | | | | 334 | 334 | 0 | 29114 | 24733 | 2279 | 333 | | | | | | | | |
| lymph node - h | | | | | | | | 332 | 706 | 0 | 1941 | 7347 | 7055 | 14451 | | | | | | | | |
| h adult SAMC 10/21/92 #17 | | | | | | | | 330 | 0 | 6514 | 6587 | 1044 | 0 | 540 | | | | | | | | |
| testis - h | | | | | | | | 328 | 7193 | 318 | 151277 | 49028 | 10433 | 8646 | | | | | | | | |
| HT 308-normal | | | | | | | | 327 | 605 | 0 | 217335 | 6223 | 320 | 8808 | | | | | | | | |
| thyroid - h | | | | | | | | 326 | 6784 | 80 | 239220 | 54119 | 10538 | 7917 | | | | | | | | |
| HT 149 - normal | | | | | | | | 321 | 197 | 61 | 901 | 2827 | 0 | 156 | | | | | | | | |
| HEPM M1 untreated | | | | | | | | 320 | 3265 | 0 | 98126 | 12132 | 3937 | 4153 | | | | | | | | |
| uterus - h | | | | | | | | 318 | 4913 | 4034 | 653304 | 26332 | 19659 | 31221 | | | | | | | | |
| testis - h | | | | | | | | 316 | 4983 | 259 | 119863 | 24236 | 13500 | 10150 | | | | | | | | |
| thyroid gland - h | | | | | | | | 314 | 2530 | 645 | 656461 | 34489 | 13185 | 36363 | | | | | | | | |
| salivary gl. - h | | | | | | | | 311 | 861 | 18154 | 18958 | 6484 | 8676 | 1955 | | | | | | | | |
| prostate - h | | | | | | | | 307 | 45 | 562 | 103424 | 14523 | 5834 | 8183 | | | | | | | | |
| pituitary gland - h | | | | | | | | 307 | 1226 | 0 | 110830 | 16053 | 2008 | 4627 | | | | | | | | |
| pancreas - h | | | | | | | | 305 | 193 | 507 | 101647 | 8652 | 2836 | 7486 | | | | | | | | |
| mammary gland - h | | | | | | | | 302 | 1134 | 700 | 1072119 | 24205 | 8178 | 3908 | | | | | | | | |
| bladder - h | | | | | | | | 302 | 4212 | 0 | 38751 | 25697 | 8508 | 7386 | | | | | | | | |
| testis - h | | | | | | | | 298 | 4247 | 11127 | 777028 | 53086 | 20243 | 35776 | | | | | | | | |
| heart - h | | | | | | | | 297 | 2925 | 1244 | 461051 | 20812 | 10344 | 10069 | | | | | | | | |
| spleen - h | | | | | | | | 296 | 55 | 118030 | 20791 | 9104 | 2059 | 53225 | | | | | | | | |
| spinal cord - h | | | | | | | | 294 | 2252 | 1632 | 326126 | 25447 | 14237 | 15358 | | | | | | | | |
| small intestine - h | | | | | | | | 292 | 155 | 115 | 366979 | 12005 | 3217 | 6660 | | | | | | | | |
| skeletal muscle - h | | | | | | | | 290 | 1375 | 1482 | 417579 | 27541 | 13618 | 30644 | | | | | | | | |
| bone marrow - h | | | | | | | | 287 | 818 | 34547 | 24111 | 3118 | 2421 | 1687 | | | | | | | | |
| adrenal gland - h | | | | | | | | 277 | 0 | 2174 | 68342 | 4719 | 2570 | 9223 | | | | | | | | |
| HPAEC | | | | | | | | 275 | 275 | 501 | 123 | 4997 | 5945 | 1414 | | | | | | | | |
| HT 302-normal | | | | | | | | 268 | 0 | 50 | 79106 | 4487 | 0 | 4489 | | | | | | | | |
| HT 303-normal | | | | | | | | 263 | 253 | 661 | 12336 | 6538 | 878 | 11880 | | | | | | | | |
| Bov-11 | | | | | | | | 239 | 239 | 1710 | 4286 | 206965 | 19722 | 1597 | | | | | | | | |
| Bov-8 | | | | | | | | 235 | 235 | 41 | 561 | 52163 | 6331 | 1048 | | | | | | | | |
| HT 12-normal | | | | | | | | 234 | 234 | 767 | 0 | 34038 | 18387 | 5366 | | | | | | | | |
| Bov-7 | | | | | | | | 233 | 233 | 0 | 1839 | 63364 | 2278 | 2074 | | | | | | | | |
| Bov-6 | | | | | | | | 231 | 231 | 391 | 2454 | 49140 | 7045 | 5702 | | | | | | | | |
| Bov-2 | | | | | | | | 229 | 229 | 466 | 1684 | 74813 | 9509 | 799 | | | | | | | | |
| Bov-1 | | | | | | | | 227 | 227 | 626 | 4954 | 63881 | 6235 | 1909 | | | | | | | | |
| testis - h | | | | | | | | 222 | 622 | 329 | 5047 | 2650 | 2386 | 54253 | </ | | | | | | | |

165
Table 3 (cont'd)

| Tissue | Tumor-ym | Normal-ym | Tumor-to | Tumor cells | Normal | Endos | p53 | SEQ 003 | ARGEO 3 | TBR | SEQ 004 | ARGEO 4 | ARGEO 5 | CARSEQ | 11 EP | SEQ 17 | PC | SEQ 14 | 15 | 16 | 17 |
|----------------------------|----------|-----------|----------|-------------|--------|-------|-----|---------|---------|---------|---------|---------|---------|--------|--------|--------|----|--------|----|----|----|
| He 578T | 155 | | | | | | | 13571 | 0 | 186624 | 345411 | 16731 | 127121 | 50761 | 46043 | 5514 | | | | | |
| MCF-7AQR-RES | 153 | | | | | | | 13420 | 1292 | 37520 | 28262 | 9797 | 5784 | 88701 | 46543 | 5182 | | | | | |
| MCF7 | 151 | | | | | | | 15337 | 1095 | 930587 | 52016 | 21779 | 15050 | 10792 | 53949 | 9415 | | | | | |
| U14 | 149 | | | | | | | 5452 | 566 | 204412 | 17124 | 10754 | 18348 | 7544 | 63303 | 4435 | | | | | |
| UACC-257 | 147 | | | | | | | 11456 | 0 | 155616 | 13667 | 10437 | 42807 | 4583 | 32000 | 8337 | | | | | |
| UACC-62 | 145 | | | | | | | 2455 | 123 | 56725 | 21571 | 11116 | 27564 | 1929 | 27441 | 4551 | | | | | |
| SK-MEL-28 | 144 | | | | | | | 4479 | 0 | 350827 | 13151 | 7222 | 23647 | 2124 | 20931 | 5624 | | | | | |
| UO-31 | 143 | | | | | | | 6347 | 0 | 217414 | 15138 | 8047 | 23531 | 1186 | 46782 | 5702 | | | | | |
| SK-MEL-5 | 142 | | | | | | | 5444 | 690 | 436886 | 16465 | 4434 | 30762 | 7045 | 29301 | 5242 | | | | | |
| WM-12 | 141 | | | | | | | 5633 | 377 | 43470 | 12308 | 4099 | 4523 | 7794 | 30992 | 3132 | | | | | |
| SK-MEL-2 | 140 | | | | | | | 2946 | 331 | 331803 | 16006 | 13917 | 13874 | 7005 | 30577 | 5799 | | | | | |
| MCT-15 | 139 | | | | | | | 1181 | 0 | 352055 | 14372 | 9250 | 17403 | 5476 | 54739 | 10141 | | | | | |
| SK-MEL-3M | 138 | | | | | | | 6590 | 0 | 403468 | 18970 | 6670 | 21327 | 8334 | 45060 | 7827 | | | | | |
| COLO 205 | 137 | | | | | | | 5349 | 0 | 384005 | 16795 | 8558 | 17491 | 4868 | 57736 | 10848 | | | | | |
| LOX MAVI | 136 | | | | | | | 4200 | 204 | 1678684 | 23713 | 10725 | 23514 | 5599 | 26018 | 7615 | | | | | |
| SW-620 | 135 | | | | | | | 11420 | 0 | 622556 | 16554 | 5952 | 18514 | 2213 | 38849 | 5702 | | | | | |
| TC-8 | 134 | | | | | | | 3536 | 1562 | 205133 | 21155 | 7332 | 9162 | 40811 | 43207 | 6844 | | | | | |
| MCT-116 | 133 | | | | | | | 3482 | 0 | 164816 | 13650 | 7385 | 8546 | 4065 | 37409 | 5317 | | | | | |
| 786-0 | 132 | | | | | | | 3264 | 0 | 206284 | 17720 | 4992 | 13644 | 5047 | 34175 | 4677 | | | | | |
| MCC-2998 | 131 | | | | | | | 6370 | 2297 | 398066 | 17568 | 5761 | 10030 | 3671 | 62363 | 8455 | | | | | |
| ACHN | 130 | | | | | | | 8652 | 177 | 84811 | 18456 | 10350 | 8438 | 4663 | 36060 | 5785 | | | | | |
| PC-3 | 129 | | | | | | | 12090 | 0 | 48624 | 14186 | 4679 | 6473 | 3508 | 35272 | 6853 | | | | | |
| RUF-353 | 128 | | | | | | | 5633 | 279 | 469833 | 21616 | 7110 | 11090 | 3324 | 40444 | 5886 | | | | | |
| DU-145 | 127 | | | | | | | 16028 | 136 | 30508 | 12131 | 3150 | 3640 | 2491 | 37717 | 3203 | | | | | |
| C6H-1 | 126 | | | | | | | 3046 | 722 | 112646 | 12748 | 8899 | 13451 | 4797 | 35251 | 6467 | | | | | |
| SR | 125 | | | | | | | 3565 | 257 | 420391 | 13247 | 3620 | 10151 | 2543 | 37859 | 4327 | | | | | |
| A498 | 124 | | | | | | | 9123 | 0 | 64349 | 18090 | 41974 | 17229 | 4374 | 39104 | 6293 | | | | | |
| RPMI 8226 | 123 | | | | | | | 17217 | 0 | 272836 | 18399 | 34181 | 26799 | 11911 | 54853 | 5696 | | | | | |
| SW-62 | 122 | | | | | | | 6263 | 232 | 202877 | 17152 | 14156 | 20787 | 1292 | 32571 | 5287 | | | | | |
| H-460 | 121 | | | | | | | 11442 | 0 | 137022 | 6968 | 5329 | 22423 | 4164 | 36440 | 4569 | | | | | |
| MOLT-4 | 120 | | | | | | | 4384 | 0 | 440040 | 12768 | 10231 | 15496 | 2066 | 28309 | 4478 | | | | | |
| OVCA-5 | 119 | | | | | | | 3620 | 368 | 1066525 | 16534 | 5752 | 11890 | 4117 | 25315 | 6235 | | | | | |
| H-562 | 118 | | | | | | | 2150 | 190 | 204733 | 14187 | 8845 | 24925 | 3340 | 54315 | 9030 | | | | | |
| OVCA-4 | 117 | | | | | | | 2856 | 3587 | 4965335 | 16528 | 8040 | 17337 | 5681 | 47598 | 9203 | | | | | |
| COF-CEM | 116 | | | | | | | 4910 | 0 | 3589707 | 21767 | 9518 | 81643 | 9569 | 36120 | 4525 | | | | | |
| OVCA-3 | 115 | | | | | | | 3311 | 0 | 551858 | 10974 | 7864 | 21926 | 5119 | 52017 | 5813 | | | | | |
| U-139 | 114 | | | | | | | 4819 | 0 | 882970 | 13841 | 4718 | 16091 | 7024 | 34963 | 4618 | | | | | |
| HOP-62 | 113 | | | | | | | 2174 | 369 | 345760 | 13736 | 5656 | 11035 | 3280 | 19576 | 4413 | | | | | |
| SP-295 | 112 | | | | | | | 11905 | 716 | 68583 | 16107 | 8440 | 7164 | 2565 | 40830 | 7967 | | | | | |
| AS-56ATCC | 111 | | | | | | | 17217 | 599 | 378650 | 27722 | 12358 | 16617 | 5358 | 47439 | 8336 | | | | | |
| U-138 | 110 | | | | | | | 3084 | 1351 | 233341 | 16600 | 6551 | 11824 | 2278 | 30243 | 5742 | | | | | |
| NCH-H22 | 109 | | | | | | | 4147 | 0 | 1126364 | 19715 | 10185 | 32962 | 3153 | 44511 | 8645 | | | | | |
| U751 | 108 | | | | | | | 8539 | 373 | 230300 | 18796 | 8509 | 12059 | 5746 | 540761 | 8260 | | | | | |
| NCH-H460 | 107 | | | | | | | 6777 | 0 | 452353 | 13800 | 6899 | 18803 | 4436 | 28826 | 5244 | | | | | |
| SNB-75 | 106 | | | | | | | 2578 | 630 | 27182 | 8638 | 72185 | 8638 | 2872 | 41196 | 4619 | | | | | |
| NCH-H22M | 105 | | | | | | | 6471 | 921 | 589327 | 19449 | 14479 | 18523 | 3322 | 49937 | 6532 | | | | | |
| SNB-19 | 104 | | | | | | | 7350 | 0 | 219881 | 17548 | 7956 | 12434 | 3103 | 50554 | 5744 | | | | | |
| NCH-H226 | 103 | | | | | | | 3259 | 310 | 108348 | 20696 | 10725 | 24197 | 3034 | 61587 | 8993 | | | | | |
| SK-OV-3 | 102 | | | | | | | 9451 | 0 | 1021760 | 15647 | 7476 | 11071 | 1281 | 33178 | 2684 | | | | | |
| NCH-H23 | 101 | | | | | | | 5614 | 371 | 109502 | 13285 | 8342 | 15724 | 2809 | 30481 | 3518 | | | | | |
| IGROV1 | 100 | | | | | | | 18802 | 768 | 313545 | 14157 | 9518 | 8579 | 2981 | 41669 | 3318 | | | | | |
| ERXV | 99 | | | | | | | 6528 | 1116 | 359818 | 18612 | 6437 | 21788 | 2010 | 25017 | 3624 | | | | | |
| OVCA-8 | 98 | | | | | | | 1781 | 814 | 167774 | 10361 | 4170 | 6061 | 3129 | 31128 | 4619 | | | | | |
| HOP-62 | 97 | | | | | | | 7808 | 0 | 317849 | 22815 | 4246 | 39600 | 3282 | 33300 | 3960 | | | | | |
| In Braxelants 3/31/92 #17 | 48 | | | | | | | 11095 | 0 | 177631 | 18163 | 6067 | 4047 | 3528 | 32090 | 4127 | | | | | |
| In Braxel SMC 18/21/92 #17 | 47 | | | | | | | 4476 | 137 | 80771 | 14410 | 126907 | 3096 | 588 | 38937 | 5335 | | | | | |
| In Braxel SMC 2/25/92 #10 | 46 | | | | | | | 13805 | 240 | 155425 | 23184 | 8658 | 14419 | 3871 | 20137 | 5742 | | | | | |
| TCGP | 26 | | | | | | | 6008 | 0 | 558454 | 15245 | 18266 | 18157 | 3439 | 22853 | 6471 | | | | | |
| AS49-1 | wt | | | | | | | 1491 | 8421 | 44505 | 11748 | 0 | 0 | 0 | 0 | 0 | | | | | |
| AS49-3 | wt | | | | | | | 139 | 4212 | 26336 | 6707 | 0 | 0 | 0 | 0 | 0 | | | | | |
| AS49-4 | wt | | | | | | | 278 | 5323 | 38473 | 10536 | 0 | 0 | 0 | 0 | 0 | | | | | |
| AS49-5 | wt | | | | | | | 480 | 2872 | 28588 | 10727 | 0 | 0 | 0 | 0 | 0 | | | | | |
| AS49-7 | wt | | | | | | | 148 | 162 | 15733 | 8786 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ERXV-1 | mutant | | | | | | | 846 | 143 | 88924 | 18784 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ERXV-4 | mutant | | | | | | | 1400 | 43690 | 78393 | 25019 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ERXV-5 | mutant | | | | | | | 935 | 934 | 22887 | 12511 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ERXV-7 | mutant | | | | | | | 0 | 0 | 58803 | 7740 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ERXV-7-1 | wt | | | | | | | 725 | 1578 | 28892 | 11042 | 0 | 0 | 0 | 0 | 0 | | | | | |
| MCF-7-1 | wt | | | | | | | 840 | 719 | 50119 | 10699 | 0 | 0 | 0 | 0 | 0 | | | | | |
| MCF-7-3 | wt | | | | | | | 607 | 6245 | 68350 | 7863 | 0 | 0 | 0 | 0 | 0 | | | | | |
| MCF-7-4 | wt | | | | | | | 839 | 1155 | 140711 | 14817 | 0 | 0 | 0 | 0 | 0 | | | | | |
| MCF-7-5 | wt | | | | | | | 224 | 1050 | 81146 | 11010 | 0 | 0 | 0 | 0 | 0 | | | | | |
| MCF-7-7 | wt | | | | | | | 0 | 1331 | 10567 | 6726 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ADR-RES-1 | mutant | | | | | | | 0 | 3885 | 51125 | 18485 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ADR-RES-3 | mutant | | | | | | | 425 | 525 | 27534 | 8062 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ADR-RES-4 | mutant | | | | | | | 0 | 15870 | 44449 | 0 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ADR-RES-5 | mutant | | | | | | | 268 | 473 | 35606 | 7549 | 0 | 0 | 0 | 0 | 0 | | | | | |
| ADR-RES-7 | mutant | | | | | | | 650 | 7502 | 12923 | 13062 | 0 | 0 | 0 | 0 | 0 | | | | | |
| WI 38-1 | wt | | | | | | | 619 | 0 | 41827 | 24067 | 0 | 0 | 0 | 0 | 0 | | | | | |
| WI 38-3 | wt | | | | | | | 508 | 217 | 40670 | 18323 | 0 | 0 | 0 | 0 | 0 | | | | | |
| WI 38-4 | wt | | | | | | | 847 | 751 | 32710 | 9317 | 0 | 0 | 0 | 0 | 0 | | | | | |
| WI 38-5 | wt | | | | | | | 1151 | 3721 | 17091 | 11387 | 0 | 0 | 0 | 0 | 0 | | | | | |
| WI 38-7 | wt | | | | | | | 218 | 4617 | 64191 | 12288 | 0 | 0 | 0 | 0 | 0 | | | | | |

| Accession | Unmod. sym | Normal sym | Unmod. fa | Unmod. calls | Normal | Endos | g33 | SEC 001 | ASEQ 3 | THRSEC 004 | ASEQ 004 | ASEQ 9 | CASEQ 11 | EPSEC 12 | PKSEC 14 | HYSEC 16 | RS |
|-------------|------------|------------|-----------|--------------|--------|-------|-----|---------|--------|------------|----------|--------|----------|----------|----------|----------|----|
| DafPeng-7 | | | | | | | | 40911 | 41531 | 1307515 | 40007 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-8 | | | | | | | | 1643 | 0 | 129784 | 31568 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-9 | | | | | | | | 1704 | 352 | 21317 | 22363 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-11 | | | | | | | | 2364 | 2910 | 54036 | 34393 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-12 | | | | | | | | 1621 | 0 | 143418 | 14764 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-10 | | | | | | | | 1137 | 11437 | 58719 | 25013 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-1 | | | | | | | | 1608 | 0 | 176675 | 67121 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-2 | | | | | | | | 778 | 282 | 80117 | 44171 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-3 | | | | | | | | 1038 | 5099 | 86419 | 23252 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-4 | | | | | | | | 44 | 3575 | 46050 | 15499 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-5 | | | | | | | | 447 | 217 | 37705 | 8958 | 0 | 0 | 0 | 0 | 0 | 0 |
| DafPeng-6 | | | | | | | | 1754 | 0 | 104757 | 34586 | 0 | 0 | 0 | 0 | 0 | 0 |
| AS49 - 6 | | | | | | | | 141 | 1851 | 30654 | 11740 | 0 | 0 | 0 | 0 | 0 | 0 |
| EKVX - 8 | | | | | | | | 2611 | 6468 | 74732 | 34175 | 0 | 0 | 0 | 0 | 0 | 0 |
| HCT-115 - 7 | | | | | | | | 459 | 0 | 45374 | 15406 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29 - 7 | | | | | | | | 360 | 845 | 68940 | 25676 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29 - 8 | | | | | | | | 293 | 5501 | 22154 | 18610 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29 - 9 | | | | | | | | 78 | 3147 | 6867 | 6481 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29 - 8 | | | | | | | | 181 | 467 | 50732 | 18019 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF530 - 7 | | | | | | | | 7368 | 375 | 15224 | 6477 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF530 - 8 | | | | | | | | wt | 0 | 57675 | 9738 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-768 - 7 | | | | | | | | 507 | 448 | 53057 | 13175 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-768-8 | | | | | | | | 907 | 0 | 30102 | 8841 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCAR-4 - 7 | | | | | | | | 691 | 1305 | 72107 | 15862 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCAR-4 - 8 | | | | | | | | 1368 | 537 | 105548 | 21701 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCAR-5 - 7 | | | | | | | | 0 | 328 | 52968 | 10750 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCAR-5 - 8 | | | | | | | | 158 | 0 | 17818 | 10967 | 0 | 0 | 0 | 0 | 0 | 0 |
| MCF-7 - 8 | | | | | | | | 555 | 740 | 24190 | 11653 | 0 | 0 | 0 | 0 | 0 | 0 |
| ADR-RES - 8 | | | | | | | | 822 | 3013 | 12554 | 17722 | 0 | 0 | 0 | 0 | 0 | 0 |
| Hut - a - 6 | | | | | | | | 0 | 2243 | 23863 | 6106 | 0 | 0 | 0 | 0 | 0 | 0 |
| SW480 - 7 | | | | | | | | 727 | 1081 | 24521 | 12811 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29 - 8 | | | | | | | | 226 | 7379 | 43102 | 8609 | 0 | 0 | 0 | 0 | 0 | 0 |
| C33A - 7 | | | | | | | | 102 | 2363 | 53891 | 10761 | 0 | 0 | 0 | 0 | 0 | 0 |
| C33A - 8 | | | | | | | | 372 | 3128 | 11403 | 8724 | 0 | 0 | 0 | | | |

167
Table 3 (cont'd)

| Tissue | Tumor - ym | Normal - ym | Tumor - to | Tumor - cala | Normal | Endose | p53 | SEQ 17 | AA | SEQ 20 | SQ | SEQ 22 | PT | SEQ 26 | AA | SEQ 29 | DR | SEQ 31 | OR | SEQ 33 | AR | SEQ 40 | MA | SEQ 44 | T |
|-------------------------|------------|-------------|------------|--------------|--------|--------|-----|--------|--------|--------|----|--------|----|--------|--------|--------|----|--------|------|--------|----|--------|----|--------|---|
| adrenal gland - h | 1 | | | | | 46820 | | 1342 | 18776 | 8931 | | | | 11409 | 24831 | 60520 | | 5991 | 4349 | | | | | | |
| lymph node - h | 2 | | | | | 94539 | | 10634 | 37310 | 14301 | | | | 80624 | 153021 | 135195 | | 334 | 2571 | | | | | | |
| bone marrow - h | 3 | | | | | 82024 | | 345 | 117785 | 11301 | | | | 51933 | 6448 | 73534 | | 0 | 794 | | | | | | |
| pancreas gland - h | 4 | | | | | 24735 | | 0 | 18847 | 1710 | | | | 2723 | 266 | 5276 | | 154 | 306 | | | | | | |
| brain - h | 5 | | | | | 54253 | | 1826 | 188461 | 6870 | | | | 925 | 1184 | 700301 | | 3190 | 2311 | | | | | | |
| pancreas - h | 6 | | | | | 71540 | | 2036 | 48828 | 7425 | | | | 7287 | 2272 | 31495 | | 4051 | 1246 | | | | | | |
| coronary artery - h | 7 | | | | | 82436 | | 104 | 298725 | 10725 | | | | 7148 | 7854 | 139678 | | 6036 | 174 | | | | | | |
| pancreas gland - h | 8 | | | | | 87365 | | 232 | 110587 | 15543 | | | | 7314 | 2404 | 74670 | | 3055 | 3472 | | | | | | |
| pancreas gland - h | 9 | | | | | 103271 | | 0 | 167692 | 22024 | | | | 3638 | 1150 | 63217 | | 7424 | 8836 | | | | | | |
| pancreas - h | 10 | | | | | 80242 | | 804 | 105453 | 8213 | | | | 8436 | 6509 | 126604 | | 1506 | 4165 | | | | | | |
| total brain - h | 11 | | | | | 45094 | | 9028 | 152875 | 10990 | | | | 12224 | 7283 | 55346 | | 5950 | 2519 | | | | | | |
| total kidney - h | 12 | | | | | 74934 | | 1446 | 64243 | 10904 | | | | 17723 | 1143 | 24080 | | 979 | 86 | | | | | | |
| prostate, h | 13 | | | | | 58677 | | 3153 | 86695 | 11342 | | | | 15732 | 2410 | 33364 | | 279 | 2130 | | | | | | |
| total liver - h | 14 | | | | | 60763 | | 0 | 122833 | 3800 | | | | 18767 | 1080 | 12909 | | 0 | 233 | | | | | | |
| salivary gland - h | 15 | | | | | 82518 | | 1478 | 187805 | 6127 | | | | 18242 | 4176 | 67498 | | 1544 | 3005 | | | | | | |
| total lung - h | 16 | | | | | 37531 | | 171 | 575843 | 2744 | | | | 1837 | 505 | 48674 | | 1077 | 2017 | | | | | | |
| skeletal muscle - h | 17 | | | | | 439811 | | 0 | 296349 | 885 | | | | 4850 | 2245 | 31329 | | 11021 | 2174 | | | | | | |
| small intestine - h | 18 | | | | | 42979 | | 1357 | 80551 | 3331 | | | | 14338 | 2021 | 21878 | | 632 | 1632 | | | | | | |
| kidney - h | 19 | | | | | 48325 | | 6757 | 77677 | 1793 | | | | 3203 | 1359 | 36570 | | 2144 | 1494 | | | | | | |
| apical cord - h | 20 | | | | | 54765 | | 1215 | 53517 | 21224 | | | | 5273 | 1063 | 21487 | | 717 | 716 | | | | | | |
| testis - h | 21 | | | | | 40332 | | 3539 | 53039 | 4414 | | | | 2272 | 1224 | 34138 | | 126 | 413 | | | | | | |
| Spleen - h | 22 | | | | | 44668 | | 0 | 129409 | 2530 | | | | 30444 | 4382 | 17845 | | 0 | 627 | | | | | | |
| lung - h | 23 | | | | | 37621 | | 571 | 103801 | 816 | | | | 25786 | 5316 | 33759 | | 0 | 125 | | | | | | |
| stomach - h | 24 | | | | | 18010 | | 344 | 37850 | 1810 | | | | 8695 | 1908 | 11633 | | 6651 | 331 | | | | | | |
| testis - h | 25 | | | | | 44850 | | 98 | 56303 | 30895 | | | | 13224 | 4542 | 332139 | | 1806 | 1333 | | | | | | |
| thyroid - h | 26 | | | | | 85252 | | 63 | 422519 | 10169 | | | | 30950 | 8722 | 120548 | | 1732 | 317 | | | | | | |
| HPAEC | 28 | | | | | 70787 | | 28 | 3134 | 2084 | | | | 2437 | 10154 | 5691 | | 120 | 0 | | | | | | |
| thyroid gland - h | 30 | | | | | 181028 | | 547 | 181028 | 8292 | | | | 4819 | 826 | 37702 | | 0 | 755 | | | | | | |
| RTPEC | 30 | | | | | 42540 | | 30 | 3012 | 5372 | | | | 4367 | 356 | 418 | | 0 | 0 | | | | | | |
| trachea - h | 31 | | | | | 78666 | | 303 | 144782 | 82321 | | | | 30464 | 3321 | 42097 | | 602 | 2353 | | | | | | |
| HAEC | 32 | | | | | 85164 | | 650 | 2147 | 3421 | | | | 0 | 3872 | 7056 | | 0 | 0 | | | | | | |
| HAEC | 33 | | | | | 65678 | | 254 | 142063 | 5371 | | | | 8755 | 1003 | 37845 | | 7649 | 3631 | | | | | | |
| pancreas - h | 34 | | | | | 51717 | | 323 | 22368 | 2129 | | | | 118 | 560 | 199 | | 242 | 0 | | | | | | |
| pancreas - h | 35 | | | | | 46443 | | 0 | 0 | 4314 | | | | 13335 | 0 | 2589 | | 0 | 1082 | | | | | | |
| lymph node - h | 36 | | | | | 64078 | | 0 | 0 | 5899 | | | | 83785 | 2110 | 7825 | | 20 | 0 | | | | | | |
| Skeletal muscle - h | 37 | | | | | 30349 | | 418 | 26839 | 26 | | | | 319 | 2085 | 817 | | 0 | 153 | | | | | | |
| total liver - h | 38 | | | | | 56121 | | 649 | 0 | 2467 | | | | 9199 | 1008 | 745 | | 947 | 250 | | | | | | |
| Heart - h | 39 | | | | | 47672 | | 0 | 2818 | 3496 | | | | 1134 | 0 | 4386 | | 492 | 0 | | | | | | |
| thyroid - h | 40 | | | | | 70722 | | 0 | 0 | 3341 | | | | 57019 | 1466 | 2672 | | 220 | 0 | | | | | | |
| Duodenum - h | 41 | | | | | 42191 | | 1414 | 0 | 4381 | | | | 4470 | 5691 | 2529 | | 180 | 2081 | | | | | | |
| Fetal brain - h | 42 | | | | | 56360 | | 570 | 0 | 6154 | | | | 4108 | 205 | 1081 | | 384 | 366 | | | | | | |
| Salivary gland - h | 43 | | | | | 35172 | | 48 | 827 | 1319 | | | | 17131 | 0 | 1205 | | 0 | 0 | | | | | | |
| testis - h | 44 | | | | | 57094 | | 129 | 294 | 2069 | | | | 13574 | 462 | 3483 | | 376 | 0 | | | | | | |
| HAEC | 45 | | | | | 12948 | | 355 | 0 | 2054 | | | | 9 | 0 | 0 | | 0 | 0 | | | | | | |
| MT218-normal | 46 | | | | | 6245 | | 77 | 0 | 246 | | | | 222 | 347 | 3271 | | 564 | 0 | | | | | | |
| MT213-normal | 47 | | | | | 16328 | | 0 | 0 | 248 | | | | 163 | 0 | 542 | | 0 | 0 | | | | | | |
| MT181-normal | 48 | | | | | 82144 | | 1094 | 0 | 27325 | | | | 6795 | 7232 | 5309 | | 1480 | 12 | | | | | | |
| Bev-13 | 49 | | | | | 50867 | | 58 | 0 | 42865 | | | | 4027 | 1119 | 422 | | 476 | 0 | | | | | | |
| Bev-12 | 50 | | | | | 27729 | | 0 | 0 | 239 | | | | 839 | 501 | 0 | | 71 | 0 | | | | | | |
| coronary artery - h | 51 | | | | | 31402 | | 290 | 0 | 0 | | | | 98 | 78 | 0 | | 0 | 0 | | | | | | |
| RTPEC | 52 | | | | | 17803 | | 334 | 334 | 8004 | | | | 9599 | 61 | 479 | | 112 | 0 | | | | | | |
| lymph node - h | 53 | | | | | 30718 | | 277 | 337 | 2691 | | | | 52871 | 2921 | 767 | | 0 | 0 | | | | | | |
| in situ SMC 1021/92 #17 | 54 | | | | | 47380 | | 237 | 0 | 788 | | | | 41 | 0 | 273 | | 54 | 0 | | | | | | |
| Fetal brain - h | 55 | | | | | 70908 | | 0 | 8377 | 20585 | | | | 10509 | 83 | 2749 | | 1212 | 0 | | | | | | |
| MT308-normal | 56 | | | | | 60974 | | 0 | 399 | 0 | | | | 10938 | 356 | 202 | | 1110 | 0 | | | | | | |
| thyroid - h | 57 | | | | | 70426 | | 326 | 0 | 634 | | | | 42378 | 26101 | 721 | | 750 | 115 | | | | | | |
| MT148 - normal | 58 | | | | | 41371 | | 416 | 0 | 0 | | | | 0 | 43 | 166 | | 325 | 0 | | | | | | |
| HEPM 34 untreated | 59 | | | | | 61910 | | 0 | 10739 | 6705 | | | | 2992 | 225 | 3580 | | 232 | 0 | | | | | | |
| lymph - h | 60 | | | | | 66453 | | 444 | 3041 | 24906 | | | | 186533 | 3035 | 4242 | | 1291 | 160 | | | | | | |
| trachea - h | 61 | | | | | 46848 | | 514 | 0 | 22803 | | | | 129836 | 7113 | 2740 | | 893 | 440 | | | | | | |
| pancreas gland - h | 62 | | | | | 44846 | | 0 | 1464 | 15691 | | | | 64896 | 5240 | 1896 | | 0 | 506 | | | | | | |
| salivary gland - h | 63 | | | | | 61687 | | 0 | 2684 | 38362 | | | | 1045 | 347 | 0 | | 0 | 0 | | | | | | |
| pancreas - h | 64 | | | | | 47609 | | 525 | 0 | 280 | | | | 25416 | 895 | 176 | | 535 | 0 | | | | | | |
| pancreas - h | 65 | | | | | 34764 | | 118 | 0 | 1592 | | | | 18211 | 815 | 376 | | 860 | 157 | | | | | | |
| pancreas gland - h | 66 | | | | | 44917 | | 305 | 0 | 631 | | | | 13630 | 1321 | 520 | | 126 | 506 | | | | | | |
| pancreas - h | 67 | | | | | 86451 | | 1168 | 0 | 8443 | | | | 102692 | 7874 | 407 | | 373 | 0 | | | | | | |
| pancreas gland - h | 68 | | | | | 72421 | | 667 | 3702 | 5722 | | | | 10239 | 184 | 478 | | 1088 | 50 | | | | | | |
| testis - h | 69 | | | | | 51918 | | 444 | 0 | 35622 | | | | 93342 | 834 | 2016 | | 1714 | 0 | | | | | | |
| testis - h | 70 | | | | | 83754 | | 0 | 1047 | 24117 | | | | 9023 | 1462 | 3474 | | 1159 | 81 | | | | | | |
| Spleen - h | 71 | | | | | 53225 | | 0 | 138 | 2172 | | | | 73586 | 6138 | 806 | | 0 | 0 | | | | | | |
| apical cord - h | 72 | | | | | 62962 | | 464 | 0 | 27722 | | | | 35430 | 3183 | 1043 | | 1150 | 155 | | | | | | |
| small intestine - h | 73 | | | | | 41621 | | 38 | 0 | 14323 | | | | 14956 | 2505 | 866 | | 0 | 133 | | | | | | |
| Skeletal muscle - h | 74 | | | | | 60372 | | 280 | 0 | 20791 | | | | 62231 | 3067 | 2424 | | 535 | 896 | | | | | | |
| bone marrow - h | 75 | | | | | 50557 | | 27 | 0 | 0 | | | | 27722 | 358 | 0 | | 0 | 0 | | | | | | |
| adrenal gland - h | 76 | | | | | 64753 | | 27 | 0 | 2305 | | | | 5560 | 59 | 0 | | 0 | 355 | | | | | | |
| HPAEC | 77 | | | | | 37169 | | 275 | 0 | 0 | | | | 1157 | 0 | 432 | | 0 | 0 | | | | | | |
| MT362-normal | 78 | | | | | 36846 | | 504 | 0 | 20358 | | | | 0 | 741 | 505 | | 0 | 0 | | | | | | |
| MT363-normal | 79 | | | | | 44114 | | 0 | 1370 | 0 | | | | 3833 | 0 | 308 | | 0 | 605 | | | | | | |
| Be | | | | | | | | | | | | | | | | | | | | | | | | | |

168
Table 3 (cont'd)

| Tissue | Tumor - ym | Normal - ym | Tumor - lo | Tumor cells | Normal | Endos | p53 | SEQ 17 | ANSEQ 20 | SEQ 22 | PTGEO 26 | ANSEQ 29 | DRSEQ 31 | DRSEQ 32 | ANSEQ 40 | MASEQ 44 | T |
|-------------------------------|------------|-------------|------------|-------------|--------|-------|-----|--------|----------|--------|----------|----------|----------|----------|----------|----------|---|
| Case 1 | | | | 167 | | | | 25641 | 11 | 01 | 7271 | 811 | 41121 | 01 | 0 | 0 | 0 |
| 786-0 | | | | 168 | | | | 43253 | 1415 | 1044 | 2462 | 2283 | 8374 | 109 | 0 | 89 | 0 |
| T-47D | | | | 169 | | | | 52705 | 0 | 4627 | 838 | 771 | 1518 | 1109 | 0 | 124 | 0 |
| Knu-3 | | | | 171 | | | | 30045 | 41 | 218 | 900 | 0 | 86 | 0 | 0 | 0 | 0 |
| CRL 1441 RNA 8/30 | | | | 181 | | | | 11952 | 0 | 486 | 1871 | 242 | 339 | 321 | 197 | 176 | 0 |
| 781T unselected + DNase | | | | 183 | | | | 21315 | 0 | 0 | 0 | 0 | 0 | 691 | 120 | 0 | 0 |
| K8 poly A+ | | | | 194 | | | | 21962 | 194 | 0 | 1630 | 2000 | 1064 | 365 | 0 | 0 | 0 |
| KHOS poly A+ | | | | 195 | | | | 30104 | 0 | 0 | 1150 | 3112 | 1662 | 115 | 0 | 30 | 0 |
| ACHN | | | | 198 | | | | 23610 | 0 | 1874 | 1898 | 523 | 874 | 750 | 371 | 126 | 0 |
| UACC-62 | | | | 200 | | | | 19193 | 130 | 99 | 1284 | 812 | 646 | 0 | 550 | 0 | 0 |
| MCF-7/ADR-RES | | | | 202 | | | | 12681 | 314 | 0 | 714 | 405 | 215 | 178 | 0 | 435 | 0 |
| UTOS (Mammary) poly A+ | | | | 204 | | | | 8406 | 0 | 0 | 1294 | 573 | 149 | 284 | 997 | 0 | 0 |
| WISH (Coloepi) poly A+ | | | | 206 | | | | 12090 | 0 | 0 | 14 | 0 | 82 | 0 | 309 | 0 | 0 |
| 458 melanoma mR1A | | | | 208 | | | | 83548 | 0 | 1041 | 3506 | 14092 | 411 | 0 | 411 | 0 | 0 |
| CCL137 RNA 3/21/85 | | | | 218 | | | | 21190 | 0 | 563 | 0 | 631 | 47 | 0 | 496 | 0 | 0 |
| W158 72h 0.5M D5, 20h 10% FBS | | | | 219 | | | | 28093 | 0 | 0 | 0 | 3727 | 0 | 149 | 176 | 134 | 0 |
| CRL 1441 + TGA (24h) 8/30 | | | | 220 | | | | 14725 | 0 | 133 | 0 | 0 | 355 | 862 | 0 | 0 | 0 |
| Kan-1 | | | | 221 | | | | 28116 | 84 | 8 | 1488 | 338 | 447 | 157 | 361 | 0 | 0 |
| Kan-2 | | | | 223 | | | | 32548 | 50 | 0 | 353 | 0 | 235 | 0 | 0 | 0 | 0 |
| Kan-4 | | | | 225 | | | | 37538 | 43 | 804 | 154 | 0 | 22 | 0 | 887 | 0 | 0 |
| HOP-82 | | | | 241 | | | | 22249 | 0 | 0 | 58 | 726 | 740 | 63 | 0 | 0 | 0 |
| MOL T-4 | | | | 242 | | | | 18708 | 0 | 1383 | 142 | 22 | 3964 | 636 | 0 | 50 | 0 |
| FKVX | | | | 243 | | | | 22457 | 387 | 303 | 1836 | 537 | 2757 | 371 | 0 | 0 | 0 |
| HL 60 | | | | 244 | | | | 33149 | 0 | 0 | 0 | 0 | 4255 | 2903 | 0 | 0 | 0 |
| HEL427 | | | | 245 | | | | 29842 | 890 | 901 | 308 | 307 | 858 | 1115 | 1154 | 1434 | 0 |
| HPM1 8226 | | | | 246 | | | | 34425 | 0 | 0 | 309 | 567 | 1614 | 134 | 222 | 60 | 0 |
| AS4B/ATCC | | | | 247 | | | | 38516 | 0 | 0 | 685 | 0 | 153 | 0 | 612 | 401 | 0 |
| SR | | | | 248 | | | | 19996 | 0 | 1351 | 0 | 354 | 733 | 0 | 897 | 62 | 0 |
| OVCA-3 | | | | 249 | | | | 27443 | 307 | 200 | 684 | 852 | 1417 | 284 | 3625 | 266 | 0 |
| HCT-15 | | | | 250 | | | | 34819 | 0 | 5278 | 813 | 1696 | 2395 | 1074 | 208 | 0 | 0 |
| OVCA-4 | | | | 251 | | | | 10333 | 478 | 1077 | 0 | 157 | 587 | 0 | 718 | 0 | 0 |
| UO-31 | | | | 252 | | | | 13456 | 0 | 115 | 0 | 242 | 757 | 0 | 0 | 116 | 0 |
| OVCA-5 | | | | 253 | | | | 50292 | 0 | 2182 | 584 | 7068 | 535 | 102 | 271 | 0 | 0 |
| SN12C | | | | 254 | | | | 39550 | 119 | 3368 | 0 | 204 | 43 | 0 | 0 | 0 | 0 |
| OVCA-6 | | | | 255 | | | | 16467 | 159 | 573 | 582 | 512 | 215 | 819 | 104 | 0 | 0 |
| LOX IMVI | | | | 256 | | | | 45485 | 0 | 18604 | 0 | 784 | 8133 | 0 | 278 | 699 | 0 |
| GROV1 | | | | 257 | | | | 36126 | 121 | 290 | 740 | 0 | 1340 | 360 | 208 | 0 | 0 |
| SK-MEL-2 | | | | 258 | | | | 34735 | 7371 | 299 | 1017 | 0 | 536 | 377 | 73 | 0 | 0 |
| SK-OV-3 | | | | 259 | | | | 17172 | 262 | 0 | 0 | 312 | 584 | 0 | 151 | 118 | 0 |
| SK-MEL-5 | | | | 260 | | | | 13827 | 212 | 508 | 0 | 141 | 339 | 0 | 54 | 0 | 0 |
| SF-539 | | | | 261 | | | | 38531 | 856 | 1771 | 974 | 853 | 3468 | 0 | 658 | 47 | 0 |
| SK-MEL-28 | | | | 262 | | | | 34495 | 0 | 337 | 617 | 1130 | 2525 | 0 | 262 | 0 | 0 |
| K-562 | | | | 263 | | | | 30125 | 198 | 11139 | 0 | 179 | 2859 | 508 | 55 | 336 | 0 |
| UACC-257 | | | | 264 | | | | 25143 | 164 | 0 | 606 | 210 | 617 | 97 | 612 | 0 | 0 |
| MYA | | | | 265 | | | | 10129 | 48 | 0 | 116 | 34 | 278 | 0 | 0 | 0 | 0 |
| MCF7 | | | | 267 | | | | 68835 | 0 | 2893 | 499 | 607 | 1109 | 2558 | 440 | 583 | 0 |
| MDA-MB-435 | | | | 269 | | | | 26815 | 0 | 678 | 815 | 40 | 503 | 5 | 0 | 0 | 0 |
| HT279 | | | | 270 | | | | 38490 | 0 | 0 | 550 | 7537 | 0 | 416 | 1472 | 276 | 0 |
| MDA-N | | | | 271 | | | | 37514 | 727 | 7083 | 0 | 0 | 482 | 2143 | 4 | 625 | 0 |
| Y79 poly A+ | | | | 273 | | | | 102505 | 972 | 2309 | 0 | 922 | 688 | 534 | 1356 | 0 | 0 |
| KHOS poly A+ | | | | 280 | | | | 38003 | 44 | 0 | 8054 | 8293 | 4347 | 3093 | 1471 | 0 | 0 |
| HTB36 24h TPA RNA 5/23 | | | | 300 | | | | 47107 | 0 | 0 | 550 | 3518 | 0 | 511 | 387 | 0 | 0 |
| HELA EXP Q31895 | | | | 313 | | | | 18329 | 0 | 0 | 0 | 0 | 311 | 290 | 0 | 0 | 0 |
| HTB36 On RNA | | | | 312 | | | | 52868 | 109 | 0 | 7168 | 17280 | 2781 | 1124 | 503 | 0 | 0 |
| HT347 | | | | 323 | | | | 40870 | 186 | 787 | 265 | 18626 | 0 | 1252 | 13 | 0 | 0 |
| 458 melanoma RNA | | | | 324 | | | | 56296 | 0 | 0 | 18772 | 5011 | 0 | 840 | 363 | 0 | 0 |
| NCI-H226 | | | | 326 | | | | 23874 | 0 | 164 | 752 | 0 | 334 | 408 | 128 | 583 | 0 |
| HOP-42 | | | | 337 | | | | 15694 | 0 | 167 | 1036 | 1027 | 2363 | 1532 | 231 | 0 | 0 |
| MDA-MB-231 | | | | 338 | | | | 35092 | 0 | 8843 | 45452 | 11567 | 18823 | 5581 | 18381 | 1619 | 0 |
| U251 | | | | 339 | | | | 33856 | 0 | 19509 | 13847 | 2782 | 63609 | 10227 | 10711 | 5160 | 0 |
| PT cells poly A+ | | | | 340 | | | | 11067 | 71 | 166 | 0 | 1453 | 0 | 0 | 0 | 48 | 0 |
| PC-3 | | | | 341 | | | | 23466 | 136 | 283 | 3466 | 925 | 813 | 386 | 0 | 262 | 0 |
| HCC-2998 | | | | 343 | | | | 17789 | 0 | 501 | 1731 | 774 | 355 | 873 | 29 | 423 | 0 |
| SW 620 | | | | 345 | | | | 15302 | 0 | 818 | 1363 | 589 | 203 | 451 | 1336 | 649 | 0 |
| HT192 | | | | 346 | | | | 42880 | 87 | 0 | 2871 | 17368 | 2232 | 1465 | 0 | 73 | 0 |
| COLO 205 | | | | 347 | | | | 12549 | 0 | 0 | 2285 | 0 | 109 | 0 | 757 | 0 | 0 |
| HT218 | | | | 348 | | | | 76025 | 0 | 0 | 383 | 8440 | 0 | 0 | 0 | 0 | 0 |
| HM-12 | | | | 349 | | | | 21716 | 0 | 1595 | 2179 | 779 | 350 | 0 | 531 | 349 | 0 |
| HT151 | | | | 350 | | | | 24568 | 894 | 8470 | 2437 | 8252 | 43 | 426 | 511 | 278 | 0 |
| A496 | | | | 351 | | | | 23633 | 0 | 183 | 4815 | 0 | 152 | 903 | 828 | 0 | 0 |
| HT293 | | | | 352 | | | | 83325 | 483 | 0 | 8725 | 15803 | 2060 | 0 | 0 | 0 | 0 |
| RUF 353 | | | | 353 | | | | 23449 | 0 | 0 | 1811 | 337 | 2050 | 212 | 425 | 0 | 0 |
| Tx-10 | | | | 354 | | | | 2285 | 268 | 5535 | 22022 | 8242 | 8629 | 2400 | 23 | 518 | 0 |
| Mame-3M | | | | 357 | | | | 74434 | 551 | 91842 | 18863 | 11098 | 31229 | 6343 | 1283 | 2753 | 0 |
| He 578T | | | | 359 | | | | 23715 | 71 | 2207 | 1808 | 924 | 1418 | 425 | 372 | 0 | 0 |
| HT213 | | | | 50 | | | | 41730 | 0 | 509 | 782 | 12170 | 286 | 0 | 0 | 0 | 0 |
| HT280 | | | | 51 | | | | 34514 | 510 | 3499 | 38948 | 259 | 6 | 0 | 0 | 0 | 0 |
| HT139 | | | | 54 | | | | 37801 | 506 | 213 | 1671 | 0 | 0 | 1041 | 55 | 143 | 0 |
| HT155 | | | | 56 | | | | 37790 | 0 | 0 | 784 | 12374 | 28 | 0 | 591 | 65 | 0 |
| HT163 | | | | 58 | | | | 58017 | 0 | 0 | 354 | 4844 | 0 | 406 | 141 | 0 | 0 |
| HT170 | | | | 70 | | | | 58964 | 781 | 0 | 7384 | 55290 | 67 | 807 | 920 | 0 | 0 |
| HT172 | | | | 62 | | | | 31376 | 81 | 0 | 871 | 3857 | 0 | 0 | 638 | 357 | 0 |
| HT136 | | | | 63 | | | | 41851 | 0 | 245 | 0 | 17086 | 0 | 171 | 0 | 0 | 0 |
| HT178 | | | | 64 | | | | 37107 | 0 | 0 | 296 | 1991 | 78 | 0 | 443 | 45 | 0 |
| HT154 | | | | 65 | | | | 13270 | 0 | 0 | 0 | 11738 | 0 | 685 | 0 | 183 | 0 |
| HT180 | | | | 66 | | | | 26571 | 81 | 0 | 901 | 3611 | 683 | 73 | 2343 | 27 | 0 |
| HT169 | | | | 67 | | | | 20113 | 0 | 0 | 2963 | 1192 | 2544 | 0 | 1630 | 0 | 0 |
| HT189 | | | | 68 | | | | 27825 | 267 | 0 | 1324 | 35 | 358 | 725 | 704 | 0 | 0 |
| HT143 | | | | 69 | | | | 20413 | 0 | 425 | 385 | 0 | 0 | 0 | 0 | 257 | 0 |
| HT190 | | | | 70 | | | | 18364 | 135 | 0 | 435 | 619 | 0 | 0 | 558 | 19 | 0 |
| HT145 | | | | 71 | | | | 27515 | 675 | 0 | 7647 | 23632 | 81 | 0 | 231 | 248 | 0 |
| HT227 | | | | 72 | | | | 30806 | 0 | 0 | 2489 | 278 | 423 | 0 | 537 | 31 | 0 |
| HT302 | | | | 73 | | | | 37705 | 0 | 0 | 1467 | 71933 | 761 | 0 | 200 | 0 | 0 |
| HT214 | | | | 74 | | | | 36927 | 475 | 0 | 131 | 18869 | 313 | 0 | 0 | 0 | 0 |
| HT317 | | | | 76 | | | | 86238 | 816 | 0 | 8015 | 82568 | 2603 | 0 | 429 | 0 | 0 |
| Neuroblastoma 84.75 11/8 | | | | 77 | | | | 30456 | 0 | 0 | 142 | 119 | 0 | 2661 | 0 | 0 | 0 |
| HT323 | | | | 78 | | | | 51648 | 187 | 538 | 0 | 12817 | 182 | 0 | 0 | 0 | 0 |
| HT327 | | | | 80 | | | | 43118 | 159 | 0 | 786 | 7545 | 87 | 160 | 821 | 0 | 0 |
| HT335 | | | | | | | | | | | | | | | | | |

169
Table 3 (cont'd)

| Tissue | Tumor - sym | Normal - sym | Tumor - to | Tumor cells | Normal | Endoc | p53 | SEQ 844 | SEQ 45 | SEQ 47 | SEQ 48 | SEQ 49 | SEQ 51 | SEQ 52 | SEQ 53 | SEQ 54 | SEQ 55 | CT |
|-----------------------------|-------------|--------------|------------|-------------|--------|-------|-----|---------|--------|--------|--------|--------|--------|--------|--------|--------|--------|-------|
| DaPeng-7 | | | | | | | | 85383 | 578 | 729 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-8 | | | | | | | | 26499 | 248 | 374 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-9 | | | | | | | | 44303 | 716 | 156 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-10 | | | | | | | | 26907 | 0 | 628 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-11 | | | | | | | | 95743 | 0 | 495 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-12 | | | | | | | | 20110 | 284 | 211 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-13 | | | | | | | | 7684 | 964 | 23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-14 | | | | | | | | 2139 | 281 | 34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-15 | | | | | | | | 606 | 1703 | 265 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-16 | | | | | | | | 26952 | 324 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-17 | | | | | | | | 42680 | 0 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-18 | | | | | | | | 33000 | 20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-19 | | | | | | | | 1966 | 23 | 90 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AS49-8 | | | | | | | | 959 | 212 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| EXVX-8 | | | | | | | | 771 | 722 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| MCT-116-7 | | | | | | | | 310 | 123 | 55 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| MCT-116-8 | | | | | | | | 310 | 0 | 144 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29-1 | | | | | | | | 0 | 0 | 25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29-7 | | | | | | | | 0 | 0 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF539-7 | | | | | | | | 1397 | 933 | 36 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF539-8 | | | | | | | | 3330 | 7 | 130 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-266-7 | | | | | | | | 17076 | 882 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-266-8 | | | | | | | | 15227 | 32 | 116 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-7 | | | | | | | | 1233 | 29 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-8 | | | | | | | | 12764 | 4 | 175 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-9 | | | | | | | | 4732 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-10 | | | | | | | | 3132 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-11 | | | | | | | | 3375 | 440 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ADR-RES-8 | | | | | | | | 1097 | 89 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HsL-8 | | | | | | | | 1022 | 717 | 22 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SW480-7 | | | | | | | | 412 | 4 | 72 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SW480-8 | | | | | | | | 0 | 162 | 10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| H1299-8 | | | | | | | | 0 | 235 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| C33A-7 | | | | | | | | 444 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| C33A-8 | | | | | | | | 28619 | 148 | 84 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| UZOS-7 | | | | | | | | 4158 | 418 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| UZOS-8 | | | | | | | | 1393 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HsL-7 | | | | | | | | 512 | 324 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HsL-8 | | | | | | | | 1504 | 41 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| WI 38-8 | | | | | | | | 0 | 0 | 70 | 5293 | 2685 | 399 | 506 | 598 | 598 | 598 | 598 |
| 456 multiple RNA | | | | | | | | 340 | 0 | 0 | 134 | 1830 | 255 | 6 | 317 | 6 | 317 | 6 |
| CRL1572 3/17/89 | | | | | | | | 642 | 0 | 0 | 189 | 5574 | 0 | 86 | 0 | 71 | 16704 | 16704 |
| Bov-4 | | | | | | | | 0 | 0 | 0 | 601 | 4678 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT368 | | | | | | | | 0 | 0 | 34 | 0 | 4412 | 215 | 0 | 0 | 0 | 0 | 0 |
| HT378 | | | | | | | | 10732 | 0 | 0 | 0 | 5567 | 8257 | 81 | 158 | 0 | 2036 | 2036 |
| HT385 | | | | | | | | 0 | 0 | 8 | 0 | 6143 | 164 | 0 | 0 | 0 | 0 | 0 |
| HT388 | | | | | | | | 53 | 0 | 0 | 0 | 3031 | 436 | 329 | 297 | 1815 | 1815 | 1815 |
| Bov-3 | | | | | | | | 0 | 0 | 56 | 34 | 1425 | 843 | 264 | 0 | 0 | 0 | 0 |
| Bov-5 | | | | | | | | 0 | 0 | 7 | 17 | 2754 | 226 | 0 | 0 | 0 | 0 | 0 |
| Bov-8 | | | | | | | | 0 | 0 | 93 | 13 | 2675 | 0 | 112 | 0 | 1299 | 1299 | 1299 |
| h keratinocytes 2/25/82 #10 | | | | | | | | 0 | 0 | 18 | 123 | 4095 | 150 | 40 | 281 | 3522 | 3522 | 3522 |
| HTB10 | | | | | | | | 0 | 0 | 39 | 23 | 4643 | 0 | 0 | 550 | 1625 | 1625 | 1625 |
| h fibroblasts 3/31/82 #12 | | | | | | | | 0 | 0 | 9 | 283 | 0 | 0 | 0 | 206 | 643 | 643 | 643 |
| prostate, h | | | | | | | | 916 | 0 | 0 | 91 | 2853 | 291 | 94 | 0 | 2243 | 2243 | 2243 |
| h keratinocytes 2/25/82 #10 | | | | | | | | 0 | 0 | 56 | 1148 | 0 | 176 | 0 | 1566 | 1566 | 1566 | 1566 |
| SA-OS (Bundy) p53 A+ | | | | | | | | 0 | 0 | 57 | 0 | 2520 | 0 | 257 | 0 | 5073 | 5073 | 5073 |
| MK p53 A+ | | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| MCT-116-3 | | | | | | | | 398 | 22 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| MCT-116-4 | | | | | | | | 438 | 1211 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| MCT-116-5 | | | | | | | | 127 | 304 | 26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| MCT-116-6 | | | | | | | | 1178 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AS49-6 | | | | | | | | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29-3 | | | | | | | | 10959 | 0 | 247 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| EXVX-6 | | | | | | | | 641 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29-4 | | | | | | | | 0 | 17 | 28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29-5 | | | | | | | | 1078 | 0 | 244 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29-6 | | | | | | | | 0 | 52 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-3 | | | | | | | | 5253 | 108 | 30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-4 | | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-5 | | | | | | | | 2869 | 271 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-6 | | | | | | | | 0 | 32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF539-3 | | | | | | | | 4462 | 146 | 140 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF539-4 | | | | | | | | 3256 | 261 | 32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF539-5 | | | | | | | | 591 | 0 | 30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF539-6 | | | | | | | | 1280 | 312 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-7 | | | | | | | | 2366 | 0 | 118 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-8 | | | | | | | | 0 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-9 | | | | | | | | 241 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVCA4-10 | | | | | | | | 60 | 6 | 120 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ADR-RES-6 | | | | | | | | 629 | 646 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| MCF-7-6 | | | | | | | | 1297 | 1521 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HsL-6 | | | | | | | | 0 | 209 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| H1299-6 | | | | | | | | 0 | 303 | 138 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SW480-3 | | | | | | | | 1137 | 629 | 67 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SW480-4 | | | | | | | | 3274 | 0 | 39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SW480-5 | | | | | | | | 885 | 175 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SW480-6 | | | | | | | | 480 | 0 | 80 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| C33A-3 | | | | | | | | 4870 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| C33A-4 | | | | | | | | 0 | 678 | 90 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| C33A-5 | | | | | | | | 3086 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| C33A-6 | | | | | | | | 0 | 0 | 59 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HsL-5 | | | | | | | | 71637 | 0 | 293 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| UZOS-3 | | | | | | | | 4526 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| UZOS-4 | | | | | | | | 7931 | 149 | 17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| UZOS-5 | | | | | | | | 0 | 0 | 49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| UZOS-6 | | | | | | | | 2111 | 0 | 242 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| WI 38-6 | | | | | | | | 0 | 0 | 57 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HsL-3 | | | | | | | | 53108 | 1252 | 246 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HsL-4 | | | | | | | | 123626 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-266-3 | | | | | | | | 5619 | 542 | 71 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-266-4 | | | | | | | | 7053 | 9567 | 399 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-266-5 | | | | | | | | 2910 | 783 | 112 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-266-6 | | | | | | | | 2789 | 1330 | 112 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPeng-13 | | | | | | | | 7166 | 761 | 45 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Michael-20 | | | | | | | | 6365 | 61 | 28 | | | | | | | | |

Table 3 (cont'd)

| Tissue | Tumor-seq | Normal-seq | Tumor - to | Tumor cells | Normal | Endos | p33 | SEQ 36 AA | SEQ 37 W | SEQ 46 AA | SEQ 63 NG | SEQ 66 CA | SEQ 68 HR | SEQ 70 R | SEQ 73 HR | SEQ 78 AA |
|----------------------------|-----------|------------|------------|-------------|--------|-------|--------|-----------|----------|-----------|-----------|-----------|-----------|----------|-----------|-----------|
| adrenal gland - h | 1 | 45395 | 10216 | 11759 | 45395 | 13724 | 10216 | 11759 | 45395 | 13724 | 10216 | 11759 | 45395 | 13724 | 10216 | 11759 |
| lymph node - h | 2 | 70206 | 24566 | 1882 | 70206 | 24566 | 33524 | 13983 | 27463 | 7405 | 313273 | 144490 | | | | |
| Bursa muscle - h | 3 | 50493 | 12341 | 24326 | 50493 | 12341 | 24326 | 26176 | 21479 | 2929 | 86136 | 105646 | | | | |
| thymus gland - h | 4 | 8569 | 209 | 3158 | 8569 | 209 | 3158 | 8569 | 209 | 3158 | 8569 | 209 | 3158 | 8569 | 209 | 3158 |
| brain - h | 5 | 33741 | 7567 | 6670 | 33741 | 7567 | 6670 | 113657 | 27844 | 3679 | 135127 | 88724 | | | | |
| pancreas - h | 6 | 36449 | 11763 | 2583 | 36449 | 11763 | 2583 | 14282 | 18704 | 3037 | 21524 | 88575 | | | | |
| coracohum - h | 7 | 69357 | 2020 | 20657 | 69357 | 2020 | 20657 | 601142 | 55613 | 1267 | 30350 | 150166 | | | | |
| testicular gland - h | 8 | 62071 | 14965 | 10920 | 62071 | 14965 | 10920 | 5242 | 70051 | 544 | 16816 | 105166 | | | | |
| testis brain - h | 9 | 66933 | 14224 | 5177 | 66933 | 14224 | 5177 | 115506 | 32885 | 5200 | 73245 | 130701 | | | | |
| muscle - h | 10 | 50118 | 15862 | 6421 | 50118 | 15862 | 6421 | 27503 | 31523 | 4144 | 29458 | 118927 | | | | |
| testis kidney - h | 11 | 45761 | 15231 | 27386 | 45761 | 15231 | 27386 | 42058 | 46683 | 3817 | 28172 | 150166 | | | | |
| testis testis - h | 12 | 28467 | 5177 | 8510 | 28467 | 5177 | 8510 | 14609 | 14609 | 6670 | 180508 | | | | | |
| testis testis - h | 13 | 31433 | 10943 | 16727 | 31433 | 10943 | 16727 | 24911 | 2114 | 47817 | 95705 | | | | | |
| salivary gl. - h | 14 | 20668 | 9416 | 1858 | 20668 | 9416 | 1858 | 19055 | 19078 | 2253 | 23301 | 180829 | | | | |
| testis lung - h | 15 | 50513 | 8396 | 6440 | 50513 | 8396 | 6440 | 27133 | 27110 | 3092 | 32855 | 175336 | | | | |
| skatular muscle - h | 16 | 34814 | 826 | 586 | 34814 | 826 | 586 | 12917 | 12917 | 7211 | 9513 | 150166 | | | | |
| heart - h | 17 | 18128 | 3037 | 3249 | 18128 | 3037 | 3249 | 17179 | 16473 | 2054 | 8417 | 108323 | | | | |
| small intestine - h | 18 | 18551 | 17299 | 1848 | 18551 | 17299 | 1848 | 9510 | 17382 | 1876 | 15605 | 254953 | | | | |
| kidney - h | 19 | 23790 | 6099 | 10880 | 23790 | 6099 | 10880 | 7368 | 38048 | 2068 | 17635 | 150166 | | | | |
| spinal cord - h | 20 | 15811 | 209 | 668 | 15811 | 209 | 668 | 29454 | 3657 | 708 | 1301 | 1301 | | | | |
| liver - h | 21 | 15711 | 8344 | 2177 | 15711 | 8344 | 2177 | 3843 | 30372 | 2113 | 10324 | 11094 | | | | |
| Spleen - h | 22 | 20778 | 16369 | 2832 | 20778 | 16369 | 2832 | 3727 | 20754 | 2087 | 4681 | 114231 | | | | |
| lung - h | 23 | 22192 | 6232 | 5714 | 22192 | 6232 | 5714 | 4773 | 38012 | 2183 | 6428 | 129686 | | | | |
| stomach - h | 24 | 18425 | 11302 | 1659 | 18425 | 11302 | 1659 | 4021 | 3464 | 2181 | 654 | 3674 | | | | |
| testis - h | 25 | 103115 | 5233 | 10154 | 103115 | 5233 | 10154 | 6256 | 10159 | 2767 | 20107 | 122629 | | | | |
| thymus - h | 26 | 57884 | 40345 | 16139 | 57884 | 40345 | 16139 | 17350 | 19356 | 4783 | 33450 | 115427 | | | | |
| HPAEC | 28 | 14426 | 8 | 996 | 14426 | 8 | 996 | 4196 | 12372 | 3412 | 0 | 83109 | | | | |
| thymus gland - h | 29 | 29474 | 2 | | 29474 | 2 | | 11280 | 11280 | 2423 | 13887 | 150166 | | | | |
| RTPEC | 30 | 508 | 13784 | 748 | 508 | 13784 | 748 | 1729 | 1861 | 15158 | 3649 | 13265 | 86954 | | | |
| trachea - h | 31 | 5137 | 74625 | 8278 | 5137 | 74625 | 8278 | 24729 | 22943 | 3340 | 21166 | 714306 | | | | |
| HPAEC | 32 | 18053 | 21362 | 28957 | 18053 | 21362 | 28957 | 0 | 25487 | 2057 | 9425 | 78553 | | | | |
| muscle - h | 33 | 1208 | 41525 | 3255 | 1208 | 41525 | 3255 | 34917 | 19410 | 2423 | 15350 | 15350 | | | | |
| HPAEC | 34 | 0 | 10916 | 752 | 0 | 10916 | 752 | 0 | 435 | 17803 | 1892 | 4218 | 72012 | | | |
| Pancreas - h | 35 | 554 | 11785 | 0 | 554 | 11785 | 0 | 3362 | 290 | 6241 | 2332 | 8669 | 128381 | | | |
| lymph node - h | 36 | 1745 | 12072 | 5592 | 1745 | 12072 | 5592 | 638 | 7598 | 3817 | 3505 | 7524 | 80329 | | | |
| Skeletal muscle - h | 37 | 621 | 5917 | 0 | 621 | 5917 | 0 | 2029 | 451 | 9051 | 7524 | 80329 | | | | |
| testis liver - h | 38 | 0 | 9143 | 362 | 0 | 9143 | 362 | 4911 | 1095 | 14308 | 2211 | 10234 | 76358 | | | |
| Heart - h | 39 | 899 | 6677 | 0 | 899 | 6677 | 0 | 6788 | 998 | 4578 | 806 | 12333 | 58107 | | | |
| Thymus h | 40 | 1510 | 11532 | 1144 | 1510 | 11532 | 1144 | 51 | 5096 | 2118 | 548 | 5848 | 5848 | | | |
| Quadriceps - h | 41 | 921 | 6294 | 530 | 921 | 6294 | 530 | 405 | 4154 | 2474 | 5176 | 55243 | | | | |
| testis brain - h | 42 | 1670 | 16310 | 0 | 1670 | 16310 | 0 | 5642 | 551 | 8086 | 3645 | 8281 | 124700 | | | |
| Spleen gl. - h | 43 | 1366 | 4850 | 0 | 1366 | 4850 | 0 | 2294 | 0 | 4275 | 1481 | 3676 | 81426 | | | |
| muscle - h | 44 | 1658 | 17351 | 0 | 1658 | 17351 | 0 | 13141 | 0 | 2101 | 10038 | 10038 | | | | |
| HT18-normal | 365 | 0 | 7137 | 125 | 0 | 7137 | 125 | 130 | 159 | 1814 | 501 | 20873 | | | | |
| HT13-normal | 361 | 0 | 8044 | 0 | 361 | 0 | 8044 | 0 | 743 | 1102 | 0 | 24903 | | | | |
| HT157-normal | 362 | 451 | 7420 | 0 | 362 | 451 | 7420 | 0 | 17 | 1661 | 336 | 30436 | | | | |
| Beas-2 | 356 | 299 | 91127 | 404 | 356 | 299 | 91127 | 404 | 5137 | 10562 | 1531 | 14920 | | | | |
| Beas-12 | 354 | 354 | 1760 | 129946 | 0 | 354 | 354 | 21 | 3012 | 4067 | 7821 | 2525 | 85002 | | | |
| coracohum - h | 344 | 0 | 4508 | 72 | 344 | 0 | 4508 | 72 | 428 | 2304 | 1611 | 30731 | | | | |
| brain - h | 342 | 0 | 1397 | 715 | 342 | 0 | 1397 | 715 | 0 | 159 | 2660 | 443 | 32872 | | | |
| RTPEC | 334 | 334 | 1042 | 10883 | 0 | 334 | 1042 | 0 | 357 | 781 | 4384 | 274 | 165461 | | | |
| lymph node - h | 332 | 153 | 12413 | 0 | 332 | 153 | 12413 | 0 | 1318 | 1259 | 3960 | 0 | 65390 | | | |
| h adult brain 10/21/02 #17 | 330 | 0 | 5643 | 0 | 330 | 0 | 5643 | 0 | 84 | 24 | 2990 | 0 | 43496 | | | |
| HT18-normal | 328 | 256 | 64197 | 537 | 328 | 256 | 64197 | 537 | 625 | 1693 | 8966 | 3760 | 95415 | | | |
| HT13-normal | 327 | 1215 | 4508 | 0 | 327 | 1215 | 4508 | 0 | 87 | 1027 | 7294 | 1 | 77941 | | | |
| thymus h | 326 | 463 | 76773 | 0 | 326 | 463 | 76773 | 0 | 287 | 5123 | 4823 | 8646 | 1169 | 89548 | | |
| HT149 - normal | 321 | 0 | 2317 | 57 | 0 | 321 | 0 | 2317 | 57 | 1 | 1316 | 2550 | 152 | 31663 | | |
| HEPM2 untreated | 320 | 1317 | 22630 | 0 | 320 | 1317 | 22630 | 0 | 846 | 214 | 5813 | 4217 | 20898 | 56244 | | |
| muscle - h | 318 | 0 | 62419 | 1852 | 318 | 0 | 62419 | 1852 | 1531 | 1203 | 30226 | 1203 | 30226 | 1203 | | |
| muscle - h | 316 | 0 | 40353 | 805 | 316 | 0 | 40353 | 805 | 1959 | 2194 | 12222 | 4302 | 140783 | 104666 | | |
| adrenal gland - h | 314 | 1 | 42997 | 0 | 314 | 1 | 42997 | 0 | 1846 | 151 | 10332 | 6811 | 96301 | 114788 | | |
| salivary gl. - h | 311 | 0 | 8898 | 0 | 311 | 0 | 8898 | 0 | 0 | 2738 | 2519 | 4532 | 10147 | | | |
| testis testis - h | 309 | 0 | 4482 | 129 | 309 | 0 | 4482 | 129 | 1622 | 2462 | 3043 | 20453 | | | | |
| adiputary gland - h | 307 | 650 | 14108 | 0 | 307 | 650 | 14108 | 0 | 214 | 235 | 1127 | 2496 | 2133 | 38646 | | |
| pancreas - h | 305 | 0 | 6503 | 0 | 305 | 0 | 6503 | 0 | 45 | 0 | 2636 | 2501 | 3386 | 55383 | | |
| mammary gland - h | 303 | 104 | 25315 | 589 | 303 | 104 | 25315 | 589 | 467 | 220 | 4367 | 4347 | 88189 | 18018 | | |
| testis - h | 302 | 1973 | 18158 | 0 | 302 | 1973 | 18158 | 0 | 3240 | 507 | 9250 | 4496 | 7521 | 65030 | | |
| testis - h | 298 | 1747 | 103561 | 7296 | 298 | 1747 | 103561 | 7296 | 489 | 1502 | 18919 | 7297 | 29073 | 148418 | | |
| testis - h | 297 | 2087 | 40917 | 2131 | 297 | 2087 | 40917 | 2131 | 330 | 1886 | 8744 | 6235 | 13181 | 110249 | | |
| Spleen - h | 296 | 206 | 8815 | 0 | 296 | 206 | 8815 | 0 | 1317 | 2880 | 3710 | 5889 | 5889 | | | |
| spinal cord - h | 294 | 205 | 48295 | 1484 | 294 | 205 | 48295 | 1484 | 52 | 1206 | 10727 | 7817 | 11556 | 112019 | | |
| small intestine - h | 292 | 280 | 7475 | 316 | 0 | 292 | 7475 | 316 | 0 | 70 | 1941 | 2922 | 8383 | 64902 | | |
| skeletal muscle - h | 290 | 1187 | 53059 | 1405 | 290 | 1187 | 53059 | 1405 | 547 | 843 | 11336 | 6645 | 29427 | 166567 | | |
| bone marrow - h | 279 | 0 | 763 | 1572 | 279 | 0 | 763 | 1572 | 0 | 0 | 1623 | 1863 | 3 | | | |
| adrenal gland - h | 277 | 0 | 6163 | 375 | 277 | 0 | 6163 | 375 | 0 | 405 | 2156 | 675 | 24322 | | | |
| HPAEC | 275 | 275 | 182 | 3675 | 56 | 275 | 182 | 3675 | 56 | 0 | 504 | 2487 | 0 | 38020 | | |
| HT392-normal | 268 | 0 | 3036 | 229 | 114 | 268 | 0 | 3036 | 229 | 114 | 267 | 0 | 407 | 52419 | | |
| HT382-normal | 266 | 0 | 2408 | 0 | 162 | 266 | 0 | 2408 | 0 | 162 | 163 | 1078 | 0 | 17286 | | |
| Beas-11 | 236 | 236 | 8272 | 8248 | 0 | 236 | 8272 | 8248 | 0 | 0 | 7268 | 408 | 18995 | 157478 | | |
| Beas-8 | 235 | 235 | 0 | 36424 | 0 | 235 | 235 | 0 | 0 | 0 | 2750 | 2873 | 1723 | 61030 | | |
| HT372-normal | 234 | 0 | 14111 | 412 | 420 | 0 | 14111 | 412 | 420 | 0 | 17 | 2430 | 603 | 80667 | | |
| Beas-7 | 233 | 233 | 343 | 2138 | 40 | 233 | 343 | 2138 | 40 | 116 | 227 | 3666 | 4362 | 7474 | | |
| Beas-2 | 231 | 231 | 778 | 4003 | 0 | 231 | 778 | 4003 | 0 | 57 | 0 | 1455 | 2754 | 3914 | 31581 | |
| Beas-1 | 229 | 229 | 197 | 5734 | 0 | 229 | 197 | 5734 | 0 | 31 | 1062 | 2069 | 2380 | 48128 | | |
| Heart - h | 227 | 227 | 1662 | 3074 | 0 | 227 | 1662 | 3074 | 0 | 145 | 196 | 1520 | 2495 | 5947 | 40717 | |
| testis - h | 225 | 0 | 4008 | 0 | 17 | 225 | 0 | 4008 | 0 | 17 | 328 | 363 | 3378 | 0 | | |
| testis - h | 215 | 0 | 1810 | 0 | 0 | 215 | 0 | 1810 | 0 | 0 | 78 | 5243 | 3097 | 1770 | 107397 | |
| stomach - h | 214 | 0 | 4816 | 0 | 0 | 214 | 0 | 4816 | 0 | 0 | 3148 | 3365 | 5934 | 81804 | | |
| testis liver - h | 213 | 0 | 2869 | 0 | 0 | 213 | 0 | 2869 | 0 | 0 | 328 | 456 | 2202 | 401 | 15566 | |
| pan | | | | | | | | | | | | | | | | |

| Tissue | Tumor-ym | Normal-ym | Tumor - To | Tumor cells | Normal | Endos | p53 | SE0 17 | AA | SE0 20 | SC | SE0 32 | PIHGE | 24 | AA | SE0 29 | OR | SE0 31 | OR | SE0 33 | AR | 40 | MA | SE0 44 | 1 |
|--------------|----------|-----------|------------|-------------|--------|-------|-----|--------|-------|--------|-------|--------|-------|-------|------|--------|----|--------|----|--------|----|----|----|--------|-----|
| h.537 | 155 | | | | | | | 45943 | 1431 | 111614 | 7266 | 2764 | 831 | 93451 | 0 | | | | | | | | | | 360 |
| MCF-7ADR-RES | 153 | | | | | | | 45543 | 0 | 784117 | 750 | 387 | 0 | 15559 | 0 | | | | | | | | | | 859 |
| MCF7 | 151 | | | | | | | 13949 | 934 | 30604 | 11924 | 2050 | 218 | 13826 | 0 | | | | | | | | | | 0 |
| UACC-251 | 149 | | | | | | | 63303 | 371 | 22226 | 15025 | 2725 | 257 | 4104 | 975 | | | | | | | | | | 73 |
| UACC-67 | 147 | | | | | | | 35000 | 1093 | 72538 | 4016 | 0 | 0 | 2232 | 0 | | | | | | | | | | 311 |
| SK-MEL-28 | 145 | | | | | | | 27441 | 0 | 7656 | 302 | 996 | 741 | 9600 | 306 | | | | | | | | | | 251 |
| UO-37 | 143 | | | | | | | 25951 | 71 | 10249 | 1402 | 2016 | 634 | 4081 | 116 | | | | | | | | | | 264 |
| SK-MEL-5 | 141 | | | | | | | 56230 | 0 | 12483 | 3316 | 644 | 1206 | 1827 | 1685 | 0 | | | | | | | | | 0 |
| KM-12 | 139 | | | | | | | 29301 | 0 | 137876 | 1862 | 110 | 260 | 18620 | 490 | | | | | | | | | | 134 |
| SK-MEL-2 | 137 | | | | | | | 30992 | 297 | 8923 | 2025 | 5 | 85 | 1287 | 0 | | | | | | | | | | 329 |
| HCT-115 | 135 | | | | | | | 30577 | 0 | 59284 | 3526 | 927 | 495 | 19563 | 0 | | | | | | | | | | 189 |
| UACC-67 | 133 | | | | | | | 64730 | 445 | 25282 | 2769 | 1572 | 287 | 8966 | 542 | 0 | | | | | | | | | 0 |
| SK-MEL-28 | 131 | | | | | | | 45060 | 1466 | 86469 | 4322 | 243 | 294 | 10449 | 226 | | | | | | | | | | 43 |
| MCF-7 | 129 | | | | | | | 57736 | 1433 | 10562 | 2540 | 486 | 0 | 5756 | 0 | | | | | | | | | | 174 |
| COLO 205 | 127 | | | | | | | 26010 | 0 | 161759 | 1512 | 680 | 567 | 26226 | 248 | | | | | | | | | | 628 |
| LOX BV1 | 125 | | | | | | | 38849 | 437 | 29529 | 750 | 203 | 198 | 8406 | 375 | | | | | | | | | | 168 |
| SW-620 | 123 | | | | | | | 43207 | 68 | 18978 | 1719 | 863 | 252 | 7086 | 42 | | | | | | | | | | 14 |
| TR-10 | 121 | | | | | | | 37499 | 345 | 18776 | 1178 | 458 | 3812 | 721 | 14 | | | | | | | | | | 68 |
| HCT 116 | 119 | | | | | | | 34175 | 0 | 27523 | 0 | 534 | 157 | 6539 | 567 | 14 | | | | | | | | | 0 |
| 786-0 | 117 | | | | | | | 62362 | 734 | 17250 | 0 | 159 | 238 | 3661 | 0 | | | | | | | | | | 641 |
| HCC-T598 | 115 | | | | | | | 26060 | 329 | 81730 | 1353 | 617 | 303 | 10449 | 25 | | | | | | | | | | 226 |
| ACHN | 113 | | | | | | | 35267 | 21 | 50837 | 1065 | 106 | 457 | 8755 | 519 | 0 | | | | | | | | | 537 |
| PC-3 | 111 | | | | | | | 49444 | 305 | 87661 | 3148 | 2477 | 2041 | 26924 | 478 | 0 | | | | | | | | | 0 |
| RFX-393 | 109 | | | | | | | 37777 | 0 | 8182 | 5153 | 140 | 400 | 15854 | 0 | | | | | | | | | | 0 |
| DL-145 | 107 | | | | | | | 35257 | 331</ | | | | | | | | | | | | | | | | |

| Tissue | Tumor - ym | Normal - ym | Tumor - 1c | Tumor cells | Normal | Endoc | p53 | SE0 17 | AA | SE0 20 | SG | SE0 27 | PT | TCG0 26 | AA | SE0 29 | DR | SE0 31 | DR | SE0 32 | AR | SE0 40 | MA | SE0 44 | T |
|-------------|------------|-------------|------------|-------------|--------|--------|-----|--------|----|--------|----|--------|----|---------|-------|--------|------|--------|------|--------|----|--------|----|--------|---|
| DaPan2-2 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 21604 | 1478 | 31565 | 2728 | 1224 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-8 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10055 | 8523 | 1767 | 1592 | 1078 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-9 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 9123 | 5898 | 25073 | 1318 | 684 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-11 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 7501 | 9216 | 14351 | 1857 | 969 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-12 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3497 | 3780 | 16748 | 1028 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-10 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 6462 | 256 | 19429 | 311 | 740 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-1 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3041 | 12536 | 8782 | 6331 | 17853 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-2 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3679 | 10389 | 6327 | 148 | 69625 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-3 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4784 | 2946 | 2782 | 3207 | 4773 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-4 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1944 | 4731 | 97 | 4214 | 903 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-5 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1170 | 20328 | 327 | 1817 | 2163 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| DaPan2-6 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 12057 | 5346 | 0 | 2639 | 1453 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| AS49 - 8 | | | | | | wt | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1464 | 9852 | 0 | 427 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ECV8 - 8 | | | | | | wt | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1513 | 2153 | 6496 | 580 | 17 | 0 | 0 | 0 | 0 | 0 | 0 |
| HCT-116 - 7 | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 242 | 2507 | 3843 | 5499 | 618 | 0 | 0 | 0 | 0 | 0 | 0 |
| HCT-116 - 8 | | | | | | wt | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 614 | 8117 | 2507 | 7631 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29 - 1 | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 420 | 3056 | 3132 | 691 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29 - 7 | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 444 | 150 | 8 | 0 | 151 | 0 | 0 | 0 | 0 | 0 | 0 |
| HT29 - 8 | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1051 | 2906 | 2178 | 0 | 1146 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF539 - 7 | | | | | | wt | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8143 | 2843 | 1015 | 208 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF539 - 8 | | | | | | wt | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 66 | 10248 | 2922 | 562 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-769-7 | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 771 | 6991 | 2712 | 1196 | 1054 | 0 | 0 | 0 | 0 | 0 | 0 |
| SF-769-8 | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1169 | 8034 | 4622 | 304 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| OVC | | | | | | | | | | | | | | | | | | | | | | | | | |

Table 3 (cont'd)

| Tissue | Tumor-ym | Normal-ym | Tumor - te | Tumor cste | Normal | Endoc | p33 | 5EO | 844 | TREQ | 45 | AA | SEQ | 47 | AA | SEQ | 48 | AA | SEQ | 49 | AA | SEQ | 51 | AA | SEQ | 52 | AA | SEQ | 54 | AA | SEQ | 55 | AA |
|----------------------|----------|-----------|------------|------------|--------|-------|-----|-------|-----|------|------|-------|-------|-------|-------|-------|-------|------|-------|-------|----|-----|----|----|-----|----|----|-----|----|----|-----|----|----|
| adrenal gland - h | 1 | 1 | | | | | | 16241 | 0 | | | | 207 | 584 | 8574 | 7198 | 2170 | 7791 | 20267 | 37691 | | | | | | | | | | | | | |
| lymph node - h | 2 | 2 | | | | | | 1985 | 0 | 237 | 0 | 5663 | 3816 | 1381 | 1112 | 45217 | | | | | | | | | | | | | | | | | |
| bone marrow - h | 3 | 3 | | | | | | 441 | 0 | 0 | 0 | 2785 | 1143 | 280 | 0 | 1250 | | | | | | | | | | | | | | | | | |
| endocrine gland - h | 4 | 4 | | | | | | 4681 | 0 | 169 | 0 | 344 | 7076 | 3342 | 838 | 8722 | 44206 | | | | | | | | | | | | | | | | |
| pancreas - h | 5 | 5 | | | | | | 368 | 0 | 0 | 0 | 7609 | 2036 | 3189 | 13785 | 85393 | | | | | | | | | | | | | | | | | |
| cardiac muscle - h | 6 | 6 | | | | | | 8608 | 0 | 70 | 0 | 6528 | 6997 | 9321 | 3226 | 36020 | | | | | | | | | | | | | | | | | |
| adipose tissue - h | 7 | 7 | | | | | | 10870 | 0 | 60 | 211 | 8163 | 2360 | 2312 | 41090 | 35806 | | | | | | | | | | | | | | | | | |
| testis - h | 8 | 8 | | | | | | 57140 | 0 | 257 | 89 | 7743 | 5614 | 3097 | 26437 | 47438 | | | | | | | | | | | | | | | | | |
| ovary - h | 9 | 9 | | | | | | 1428 | 0 | 51 | 87 | 8163 | 2360 | 2312 | 41090 | 35806 | | | | | | | | | | | | | | | | | |
| placenta - h | 10 | 10 | | | | | | 2337 | 0 | 233 | 0 | 9334 | 8433 | 1375 | 30344 | 73605 | | | | | | | | | | | | | | | | | |
| total kidney - h | 11 | 11 | | | | | | 2093 | 0 | 174 | 0 | 7673 | 3767 | 334 | 5551 | 21151 | | | | | | | | | | | | | | | | | |
| prostate - h | 12 | 12 | | | | | | 2978 | 0 | 196 | 160 | 8958 | 1682 | 810 | 4385 | 47119 | | | | | | | | | | | | | | | | | |
| testis - h | 13 | 13 | | | | | | 0 | 0 | 130 | 0 | 9005 | 3418 | 1128 | 5531 | 26923 | | | | | | | | | | | | | | | | | |
| salivary gland - h | 14 | 14 | | | | | | 6390 | 0 | 319 | 348 | 10713 | 6378 | 1758 | 20642 | 64752 | | | | | | | | | | | | | | | | | |
| total lung - h | 15 | 15 | | | | | | 32869 | 0 | 0 | 0 | 5708 | 1942 | 1193 | 2028 | 14512 | | | | | | | | | | | | | | | | | |
| chondrial muscle - h | 16 | 16 | | | | | | 6442 | 0 | 101 | 101 | 5123 | 472 | 1022 | 2810 | 16767 | | | | | | | | | | | | | | | | | |
| heart - h | 17 | 17 | | | | | | 2753 | 0 | 86 | 144 | 1037 | 2965 | 443 | 4127 | 22790 | | | | | | | | | | | | | | | | | |
| small intestine - h | 18 | 18 | | | | | | 0 | 0 | 181 | 225 | 6344 | 2052 | 761 | 7039 | 31645 | | | | | | | | | | | | | | | | | |
| kidney - h | 19 | 19 | | | | | | 0 | 0 | 136 | 0 | 5679 | 2646 | 558 | 1254 | 14331 | | | | | | | | | | | | | | | | | |
| spinal cord - h | 20 | 20 | | | | | | 8349 | 0 | 0 | 0 | 4814 | 0 | 633 | 0 | 15760 | | | | | | | | | | | | | | | | | |
| testis - h | 21 | 21 | | | | | | 2363 | 0 | 0 | 196 | 5447 | 3308 | 631 | 997 | 18460 | | | | | | | | | | | | | | | | | |
| spleen - h | 22 | 22 | | | | | | 2011 | 0 | 105 | 177 | 3966 | 2134 | 673 | 3438 | 24017 | | | | | | | | | | | | | | | | | |
| lung - h | 23 | 23 | | | | | | 2652 | 0 | 125 | 0 | 3808 | 812 | 281 | 1243 | 17607 | | | | | | | | | | | | | | | | | |
| stomach - h | 24 | 24 | | | | | | 20445 | 0 | 1160 | 200 | 5630 | 8251 | 11864 | 32178 | 49517 | | | | | | | | | | | | | | | | | |
| intestine - h | 25 | 25 | | | | | | 1202 | 0 | 47 | 22 | 6191 | 4925 | 1638 | 11408 | 85005 | | | | | | | | | | | | | | | | | |
| thyroid - h | 26 | 26 | | | | | | 356 | 0 | 35 | 35 | 5356 | 0 | 0 | 0 | 9076 | | | | | | | | | | | | | | | | | |
| HPAEC | 27 | 27 | | | | | | 805 | 0 | 158 | 0 | 5306 | 1800 | 556 | 8454 | 27900 | | | | | | | | | | | | | | | | | |
| HPAEC | 28 | 28 | | | | | | 188 | 0 | 19 | 98 | 4188 | 10744 | 64 | 0 | 0 | | | | | | | | | | | | | | | | | |
| HPAEC | 29 | 29 | | | | | | 3411 | 0 | 79 | 0 | 6162 | 4192 | 1507 | 9586 | 34950 | | | | | | | | | | | | | | | | | |
| HPAEC | 30 | 30 | | | | | | 0 | 0 | 33 | 168 | 4406 | 144 | 99 | 393 | 9796 | | | | | | | | | | | | | | | | | |
| HPAEC | 31 | 31 | | | | | | 3981 | 0 | 62 | 307 | 7257 | 7343 | 1366 | 7394 | 36540 | | | | | | | | | | | | | | | | | |
| HPAEC | 32 | 32 | | | | | | 194 | 0 | 26 | 70 | 5751 | 6835 | 219 | 661 | 21419 | | | | | | | | | | | | | | | | | |
| HPAEC | 33 | 33 | | | | | | 520 | 0 | 0 | 0 | 6288 | 0 | 0 | 0 | 0 | | | | | | | | | | | | | | | | | |
| HPAEC | 34 | 34 | | | | | | 1518 | 0 | 116 | 0 | 5373 | 20984 | 115 | 9607 | 25025 | | | | | | | | | | | | | | | | | |
| HPAEC | 35 | 35 | | | | | | 399 | 0 | 14 | 0 | 3413 | 0 | 31 | 0 | 2243 | | | | | | | | | | | | | | | | | |
| HPAEC | 36 | 36 | | | | | | 8035 | 0 | 0 | 0 | 6081 | 9072 | 134 | 0 | 23611 | | | | | | | | | | | | | | | | | |
| HPAEC | 37 | 37 | | | | | | 0 | 0 | 17 | 33 | 4065 | 10004 | 41 | 0 | 2701 | | | | | | | | | | | | | | | | | |
| HPAEC | 38 | 38 | | | | | | 100 | 0 | 0 | 67 | 4633 | 8751 | 0 | 0 | 26458 | | | | | | | | | | | | | | | | | |
| HPAEC | 39 | 39 | | | | | | 92 | 0 | 0 | 0 | 3090 | 0 | 0 | 0 | 2975 | | | | | | | | | | | | | | | | | |
| HPAEC | 40 | 40 | | | | | | 11623 | 0 | 0 | 0 | 5663 | 8294 | 145 | 0 | 18626 | | | | | | | | | | | | | | | | | |
| HPAEC | 41 | 41 | | | | | | 0 | 0 | 407 | 5511 | 1427 | 0 | 0 | 0 | 16266 | | | | | | | | | | | | | | | | | |
| HPAEC | 42 | 42 | | | | | | 1732 | 0 | 27 | 53 | 7444 | 19562 | 115 | 12733 | 22793 | | | | | | | | | | | | | | | | | |
| HPAEC | 43 | 43 | | | | | | 671 | 0 | 0 | 0 | 301 | 0 | 0 | 0 | 0 | | | | | | | | | | | | | | | | | |
| HPAEC | 44 | 44 | | | | | | 365 | 0 | 0 | 0 | 225 | 0 | 32 | 0 | 482 | | | | | | | | | | | | | | | | | |
| HPAEC | 45 | 45 | | | | | | 363 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | | | | | | | | | | | | | | | | |
| HPAEC | 46 | 46 | | | | | | 361 | 0 | 0 | 0 | 17 | 1307 | 387 | 21 | 0 | 8452 | | | | | | | | | | | | | | | | |
| HPAEC | 47 | 47 | | | | | | 2196 | 0 | 0 | 403 | 8850 | 2907 | 248 | 0 | 6825 | | | | | | | | | | | | | | | | | |
| HPAEC | 48 | 48 | | | | | | 354 | 354 | 6027 | 0 | 40 | 0 | 8406 | 346 | 116 | 330 | 2534 | | | | | | | | | | | | | | | |
| HPAEC | 49 | 49 | | | | | | 344 | 0 | 0 | 71 | 1962 | 4871 | 30 | 360 | 6728 | | | | | | | | | | | | | | | | | |
| HPAEC | 50 | 50 | | | | | | 342 | 0 | 0 | 0 | 1829 | 1178 | 0 | 2981 | 7542 | | | | | | | | | | | | | | | | | |
| HPAEC | 51 | 51 | | | | | | 334 | 334 | 0 | 0 | 200 | 9040 | 117 | 0 | 0 | | | | | | | | | | | | | | | | | |
| HPAEC | 52 | 52 | | | | | | 332 | 0 | 0 | 6 | 0 | 4034 | 0 | 521 | 0 | 27619 | | | | | | | | | | | | | | | | |
| HPAEC | 53 | 53 | | | | | | 330 | 0 | 0 | 0 | 396 | 4452 | 0 | 87 | 0 | 5511 | | | | | | | | | | | | | | | | |
| HPAEC | 54 | 54 | | | | | | 328 | 0 | 0 | 26 | 10 | 7086 | 29 | 603 | 43501 | 15417 | | | | | | | | | | | | | | | | |
| HPAEC | 55 | 55 | | | | | | 326 | 0 | 0 | 118 | 176 | 4857 | 0 | 0 | 42 | 409 | | | | | | | | | | | | | | | | |
| HPAEC | 56 | 56 | | | | | | 324 | 0 | 0 | 0 | 250 | 5583 | 0 | 625 | 547 | 78037 | | | | | | | | | | | | | | | | |
| HPAEC | 57 | 57 | | | | | | 321 | 0 | 0 | 0 | 3459 | 0 | 0 | 0 | 7102 | | | | | | | | | | | | | | | | | |
| HPAEC | 58 | 58 | | | | | | 318 | 0 | 0 | 6 | 3821 | 0 | 0 | 0 | 3657 | | | | | | | | | | | | | | | | | |
| HPAEC | 59 | 59 | | | | | | 316 | 0 | 0 | 313 | 0 | 6339 | 8543 | 0 | 0 | 66364 | | | | | | | | | | | | | | | | |
| HPAEC | 60 | 60 | | | | | | 314 | 0 | 0 | 29 | 164 | 4057 | 2227 | 167 | 5551 | 22075 | | | | | | | | | | | | | | | | |
| HPAEC | 61 | 61 | | | | | | 312 | 0 | 0 | 229 | 176 | 5272 | 4413 | 343 | 58830 | | | | | | | | | | | | | | | | | |
| HPAEC | 62 | 62 | | | | | | 310 | 0 | 0 | 84 | 0 | 5050 | 810 | 27 | 0 | 17721 | | | | | | | | | | | | | | | | |
| HPAEC | 63 | 63 | | | | | | 308 | 0 | 0 | 0 | 5456 | 708 | 0 | 0 | 11078 | | | | | | | | | | | | | | | | | |
| HPAEC | 64 | 64 | | | | | | 307 | 0 | 0 | 0 | 370 | 2428 | 0 | 66 | 205 | | | | | | | | | | | | | | | | | |
| HPAEC | 65 | 65 | | | | | | 305 | 0 | 0 | 34 | 250 | 5133 | 2262 | 58 | | | | | | | | | | | | | | | | | | |

174
Table 3 (cont'd)

| Accession | Tumor cpm | Normal cpm | Tumor - 1a | Tumor cells | Normal | Endos | p33 | SEQ 44 | TREG | 45 | AA | SEQ 47 | AA | SEQ 48 | AA | SEQ 49 | AA | SEQ 50 | AA | SEQ 51 | AA | SEQ 52 | AA | SEQ 53 | AA | SEQ 54 | AA | SEQ 55 | AA | SEQ 56 | AA | SEQ 57 | AA | SEQ 58 | AA | SEQ 59 | AA | SEQ 60 | AA | SEQ 61 | AA | SEQ 62 | AA | SEQ 63 | AA | SEQ 64 | AA | SEQ 65 | AA | SEQ 66 | AA | SEQ 67 | AA | SEQ 68 | AA | SEQ 69 | AA | SEQ 70 | AA | SEQ 71 | AA | SEQ 72 | AA | SEQ 73 | AA | SEQ 74 | AA | SEQ 75 | AA | SEQ 76 | AA | SEQ 77 | AA | SEQ 78 | AA | SEQ 79 | AA | SEQ 80 | AA | SEQ 81 | AA | SEQ 82 | AA | SEQ 83 | AA | SEQ 84 | AA | SEQ 85 | AA | SEQ 86 | AA | SEQ 87 | AA | SEQ 88 | AA | SEQ 89 | AA | SEQ 90 | AA | SEQ 91 | AA | SEQ 92 | AA | SEQ 93 | AA | SEQ 94 | AA | SEQ 95 | AA | SEQ 96 | AA | SEQ 97 | AA | SEQ 98 | AA | SEQ 99 | AA | SEQ 100 | AA | SEQ 101 | AA | SEQ 102 | AA | SEQ 103 | AA | SEQ 104 | AA | SEQ 105 | AA | SEQ 106 | AA | SEQ 107 | AA | SEQ 108 | AA | SEQ 109 | AA | SEQ 110 | AA | SEQ 111 | AA | SEQ 112 | AA | SEQ 113 | AA | SEQ 114 | AA | SEQ 115 | AA | SEQ 116 | AA | SEQ 117 | AA | SEQ 118 | AA | SEQ 119 | AA | SEQ 120 | AA | SEQ 121 | AA | SEQ 122 | AA | SEQ 123 | AA | SEQ 124 | AA | SEQ 125 | AA | SEQ 126 | AA | SEQ 127 | AA | SEQ 128 | AA | SEQ 129 | AA | SEQ 130 | AA | SEQ 131 | AA | SEQ 132 | AA | SEQ 133 | AA | SEQ 134 | AA | SEQ 135 | AA | SEQ 136 | AA | SEQ 137 | AA | SEQ 138 | AA | SEQ 139 | AA | SEQ 140 | AA | SEQ 141 | AA | SEQ 142 | AA | SEQ 143 | AA | SEQ 144 | AA | SEQ 145 | AA | SEQ 146 | AA | SEQ 147 | AA | SEQ 148 | AA | SEQ 149 | AA | SEQ 150 | AA | SEQ 151 | AA | SEQ 152 | AA | SEQ 153 | AA | SEQ 154 | AA | SEQ 155 | AA | SEQ 156 | AA | SEQ 157 | AA | SEQ 158 | AA | SEQ 159 | AA | SEQ 160 | AA | SEQ 161 | AA | SEQ 162 | AA | SEQ 163 | AA | SEQ 164 | AA | SEQ 165 | AA | SEQ 166 | AA | SEQ 167 | AA | SEQ 168 | AA | SEQ 169 | AA | SEQ 170 | AA | SEQ 171 | AA | SEQ 172 | AA | SEQ 173 | AA | SEQ 174 | AA | SEQ 175 | AA | SEQ 176 | AA | SEQ 177 | AA | SEQ 178 | AA | SEQ 179 | AA | SEQ 180 | AA | SEQ 181 | AA | SEQ 182 | AA | SEQ 183 | AA | SEQ 184 | AA | SEQ 185 | AA | SEQ 186 | AA | SEQ 187 | AA | SEQ 188 | AA | SEQ 189 | AA | SEQ 190 | AA | SEQ 191 | AA | SEQ 192 | AA | SEQ 193 | AA | SEQ 194 | AA | SEQ 195 | AA | SEQ 196 | AA | SEQ 197 | AA | SEQ 198 | AA | SEQ 199 | AA | SEQ 200 | AA | SEQ 201 | AA | SEQ 202 | AA | SEQ 203 | AA | SEQ 204 | AA | SEQ 205 | AA | SEQ 206 | AA | SEQ 207 | AA | SEQ 208 | AA | SEQ 209 | AA | SEQ 210 | AA | SEQ 211 | AA | SEQ 212 | AA | SEQ 213 | AA | SEQ 214 | AA | SEQ 215 | AA | SEQ 216 | AA | SEQ 217 | AA | SEQ 218 | AA | SEQ 219 | AA | SEQ 220 | AA | SEQ 221 | AA | SEQ 222 | AA | SEQ 223 | AA | SEQ 224 | AA | SEQ 225 | AA | SEQ 226 | AA | SEQ 227 | AA | SEQ 228 | AA | SEQ 229 | AA | SEQ 230 | AA | SEQ 231 | AA | SEQ 232 | AA | SEQ 233 | AA | SEQ 234 | AA | SEQ 235 | AA | SEQ 236 | AA | SEQ 237 | AA | SEQ 238 | AA | SEQ 239 | AA | SEQ 240 | AA | SEQ 241 | AA | SEQ 242 | AA | SEQ 243 | AA | SEQ 244 | AA | SEQ 245 | AA | SEQ 246 | AA | SEQ 247 | AA | SEQ 248 | AA | SEQ 249 | AA | SEQ 250 | AA | SEQ 251 | AA | SEQ 252 | AA | SEQ 253 | AA | SEQ 254 | AA | SEQ 255 | AA | SEQ 256 | AA | SEQ 257 | AA | SEQ 258 | AA | SEQ 259 | AA | SEQ 260 | AA | SEQ 261 | AA | SEQ 262 | AA | SEQ 263 | AA | SEQ 264 | AA | SEQ 265 | AA | SEQ 266 | AA | SEQ 267 | AA | SEQ 268 | AA | SEQ 269 | AA | SEQ 270 | AA | SEQ 271 | AA | SEQ 272 | AA | SEQ 273 | AA | SEQ 274 | AA | SEQ 275 | AA | SEQ 276 | AA | SEQ 277 | AA | SEQ 278 | AA | SEQ 279 | AA | SEQ 280 | AA | SEQ 281 | AA | SEQ 282 | AA | SEQ 283 | AA | SEQ 284 | AA | SEQ 285 | AA | SEQ 286 | AA | SEQ 287 | AA | SEQ 288 | AA | SEQ 289 | AA | SEQ 290 | AA | SEQ 291 | AA | SEQ 292 | AA | SEQ 293 | AA | SEQ 294 | AA | SEQ 295 | AA | SEQ 296 | AA | SEQ 297 | AA | SEQ 298 | AA | SEQ 299 | AA | SEQ 300 | AA | SEQ 301 | AA | SEQ 302 | AA | SEQ 303 | AA | SEQ 304 | AA | SEQ 305 | AA | SEQ 306 | AA | SEQ 307 | AA | SEQ 308 | AA | SEQ 309 | AA | SEQ 310 | AA | SEQ 311 | AA | SEQ 312 | AA | SEQ 313 | AA | SEQ 314 | AA | SEQ 315 | AA | SEQ 316 | AA | SEQ 317 | AA | SEQ 318 | AA | SEQ 319 | AA | SEQ 320 | AA | SEQ 321 | AA | SEQ 322 | AA | SEQ 323 | AA | SEQ 324 | AA | SEQ 325 | AA | SEQ 326 | AA | SEQ 327 | AA | SEQ 328 | AA | SEQ 329 | AA | SEQ 330 | AA | SEQ 331 | AA | SEQ 332 | AA | SEQ 333 | AA | SEQ 334 | AA | SEQ 335 | AA | SEQ 336 | AA | SEQ 337 | AA | SEQ 338 | AA | SEQ 339 | AA | SEQ 340 | AA | SEQ 341 | AA | SEQ 342 | AA | SEQ 343 | AA | SEQ 344 | AA | SEQ 345 | AA | SEQ 346 | AA | SEQ 347 | AA | SEQ 348 | AA | SEQ 349 | AA | SEQ 350 | AA | SEQ 351 | AA | SEQ 352 | AA | SEQ 353 | AA | SEQ 354 | AA | SEQ 355 | AA | SEQ 356 | AA | SEQ 357 | AA | SEQ 358 | AA | SEQ 359 | AA | SEQ 360 | AA | SEQ 361 | AA | SEQ 362 | AA | SEQ 363 | AA | SEQ 364 | AA | SEQ 365 | AA | SEQ 366 | AA | SEQ 367 | AA | SEQ 368 | AA | SEQ 369 | AA | SEQ 370 | AA | SEQ 371 | AA | SEQ 372 | AA | SEQ 373 | AA | SEQ 374 | AA | SEQ 375 | AA | SEQ 376 | AA | SEQ 377 | AA | SEQ 378 | AA | SEQ 379 | AA | SEQ 380 | AA | SEQ 381 | AA | SEQ 382 | AA | SEQ 383 | AA | SEQ 384 | AA | SEQ 385 | AA | SEQ 386 | AA | SEQ 387 | AA | SEQ 388 | AA | SEQ 389 | AA | SEQ 390 | AA | SEQ 391 | AA | SEQ 392 | AA | SEQ 393 | AA | SEQ 394 | AA | SEQ 395 | AA | SEQ 396 | AA | SEQ 397 | AA | SEQ 398 | AA | SEQ 399 | AA | SEQ 400 | AA | SEQ 401 | AA | SEQ 402 | AA | SEQ 403 | AA | SEQ 404 | AA | SEQ 405 | AA | SEQ 406 | AA | SEQ 407 | AA | SEQ 408 | AA | SEQ 409 | AA | SEQ 410 | AA | SEQ 411 | AA | SEQ 412 | AA | SEQ 413 | AA | SEQ 414 | AA | SEQ 415 | AA | SEQ 416 | AA | SEQ 417 | AA | SEQ 418 | AA | SEQ 419 | AA | SEQ 420 | AA | SEQ 421 | AA | SEQ 422 | AA | SEQ 423 | AA | SEQ 424 | AA | SEQ 425 | AA | SEQ 426 | AA | SEQ 427 | AA | SEQ 428 | AA | SEQ 429 | AA | SEQ 430 | AA | SEQ 431 | AA | SEQ 432 | AA | SEQ 433 | AA | SEQ 434 | AA | SEQ 435 | AA | SEQ 436 | AA | SEQ 437 | AA | SEQ 438 | AA | SEQ 439 | AA | SEQ 440 | AA | SEQ 441 | AA | SEQ 442 | AA | SEQ 443 | AA | SEQ 444 | AA | SEQ 445 | AA | SEQ 446 | AA | SEQ 447 | AA | SEQ 448 | AA | SEQ 449 | AA | SEQ 450 | AA | SEQ 451 | AA | SEQ 452 | AA | SEQ 453 | AA | SEQ 454 | AA | SEQ 455 | AA | SEQ 456 | AA | SEQ 457 | AA | SEQ 458 | AA | SEQ 459 | AA | SEQ 460 | AA | SEQ 461 | AA | SEQ 462 | AA | SEQ 463 | AA | SEQ 464 | AA | SEQ 465 | AA | SEQ 466 | AA | SEQ 467 | AA | SEQ 468 | AA | SEQ 469 | AA | SEQ 470 | AA | SEQ 471 | AA | SEQ 472 | AA | SEQ 473 | AA | SEQ 474 | AA | SEQ 475 | AA | SEQ 476 | AA | SEQ 477 | AA | SEQ 478 | AA | SEQ 479 | AA | SEQ 480 | AA | SEQ 481 | AA | SEQ 482 | AA | SEQ 483 | AA | SEQ 484 | AA | SEQ 485 | AA | SEQ 486 | AA | SEQ 487 | AA | SEQ 488 | AA | SEQ 489 | AA | SEQ 490 | AA | SEQ 491 | AA | SEQ 492 | AA | SEQ 493 | AA | SEQ 494 | AA | SEQ 495 | AA | SEQ 496 | AA | SEQ 497 | AA | SEQ 498 | AA | SEQ 499 | AA | SEQ 500 | AA | SEQ 501 | AA | SEQ 502 | AA | SEQ 503 | AA | SEQ 504 | AA | SEQ 505 | AA | SEQ 506 | AA | SEQ 507 | AA | SEQ 508 | AA | SEQ 509 | AA | SEQ 510 | AA | SEQ 511 | AA | SEQ 512 | AA | SEQ 513 | AA | SEQ 514 | AA | SEQ 515 | AA | SEQ 516 | AA | SEQ 517 | AA | SEQ 518 | AA | SEQ 519 | AA | SEQ 520 | AA | SEQ 521 | AA | SEQ 522 | AA | SEQ 523 | AA | SEQ 524 | AA | SEQ 525 | AA | SEQ 526 | AA | SEQ 527 | AA | SEQ 528 | AA | SEQ 529 | AA | SEQ 530 | AA | SEQ 531 | AA | SEQ 532 | AA | SEQ 533 | AA | SEQ 534 | AA | SEQ 535 | AA | SEQ 536 | AA | SEQ 537 | AA | SEQ 538 | AA | SEQ 539 | AA | SEQ 540 | AA | SEQ 541 | AA | SEQ 542 | AA | SEQ 543 | AA | SEQ 544 | AA | SEQ 545 | AA | SEQ 546 | AA | SEQ 547 | AA | SEQ 548 | AA | SEQ 549 | AA | SEQ 550 | AA | SEQ 551 | AA | SEQ 552 | AA | SEQ 553 | AA | SEQ 554 | AA | SEQ 555 | AA | SEQ 556 | AA | SEQ 557 | AA | SEQ 558 | AA | SEQ 559 | AA | SEQ 560 | AA | SEQ 561 | AA | SEQ 562 | AA | SEQ 563 | AA | SEQ 564 | AA | SEQ 565 | AA | SEQ 566 | AA | SEQ 567 | AA | SEQ 568 | AA | SEQ 569 | AA | SEQ 570 | AA | SEQ 571 | AA | SEQ 572 | AA | SEQ 573 | AA | SEQ 574 | AA | SEQ 575 | AA | SEQ 576 | AA | SEQ 577 | AA | SEQ 578 | AA | SEQ 579 | AA | SEQ 580 | AA | SEQ 581 | AA | SEQ 582 | AA | SEQ 583 | AA | SEQ 584 | AA | SEQ 585 | AA | SEQ 586 | AA | SEQ 587 | AA | SEQ 588 | AA | SEQ 589 | AA | SEQ 590 | AA | SEQ 591 | AA | SEQ 592 | AA | SEQ 593 | AA | SEQ 594 | AA | SEQ 595 | AA | SEQ 596 | AA | SEQ 597 | AA | SEQ 598 | AA | SEQ 599 | AA | SEQ 600 | AA | SEQ 601 | AA | SEQ 602 | AA | SEQ 603 | AA | SEQ 604 | AA | SEQ 605 | AA | SEQ 606 | AA | SEQ 607 | AA | SEQ 608 | AA | SEQ 609 | AA | SEQ 610 | AA | SEQ 611 | AA | SEQ 612 | AA | SEQ 613 | AA | SEQ 614 | AA | SEQ 615 | AA | SEQ 616 | AA | SEQ 617 | AA | SEQ 618 | AA | SEQ 619 | AA | SEQ 620 | AA | SEQ 621 | AA | SEQ 622 | AA | SEQ 623 | AA | SEQ 624 | AA | SEQ 625 | AA | SEQ 626 | AA | SEQ 627 | AA | SEQ 628 | AA | SEQ 629 | AA | SEQ 630 | AA | SEQ 631 | AA | SEQ 632 | AA | SEQ 633 | AA | SEQ 634 | AA | SEQ 635 | AA | SEQ 636 | AA | SEQ 637 | AA | SEQ 638 | AA | SEQ 639 | AA | SEQ 640 | AA | SEQ 641 | AA | SEQ 642 | AA | SEQ 643 | AA | SEQ 644 | AA | SEQ 645 | AA | SEQ 646 | AA | SEQ 647 | AA | SEQ 648 | AA | SEQ 649 | AA | SEQ 650 | AA | SEQ 651 | AA | SEQ 652 | AA | SEQ 653 | AA | SEQ 654 | AA | SEQ 655 | AA | SEQ 656 | AA | SEQ 657 | AA | SEQ 658 | AA | SEQ 659 | AA | SEQ 660 | AA | SEQ 661 | AA | SEQ 662 | AA | SEQ 663 | AA | SEQ 664 | AA | SEQ 665 | AA | SEQ 666 | AA | SEQ 667 | AA | SEQ 668 | AA | SEQ 669 | AA | SEQ 670 | AA | SEQ 671 | AA | SEQ 672 | AA | SEQ 673 | AA | SEQ 674 | AA | SEQ 675 | AA | SEQ 676 | AA | SEQ 677 | AA | SEQ 678 | AA | SEQ 679 | AA | SEQ 680 | AA | SEQ 681 | AA | SEQ 682 | AA | SEQ 683 | AA | SEQ 684 | AA | SEQ 685 | AA | SEQ 686 | AA | SEQ 687 | AA | SEQ 688 | AA | SEQ 689 | AA | SEQ 690 | AA | SEQ 691 | AA | SEQ 692 | AA | SEQ 693 | AA | SEQ 694 | AA | SEQ 695 | AA | SEQ 696 | AA | SEQ 697 | AA | SEQ 698 | AA | SEQ 699 | AA | SEQ 700 | AA | SEQ 701 | AA | SEQ 702 | AA | SEQ 703 | AA | SEQ 704 | AA | SEQ 705 | AA | SEQ 706 | AA | SEQ 707 | AA | SEQ 708 | AA | SEQ 709 | AA | SEQ 710 | AA | SEQ 711 | AA | SEQ 712 | AA | SEQ 713 | AA | SEQ 714 | AA | SEQ 715 | AA | SEQ 716 | AA | SEQ 717 | AA | SEQ 718 | AA | SEQ 719 | AA | SEQ 720 | AA | SEQ 721 | AA | SEQ 722 | AA | SEQ 723 | AA | SEQ 724 | AA | SEQ 725 | AA | SEQ 726 | AA | SEQ 727 | AA | SEQ 728 | AA | SEQ 729 | AA | SEQ 730 | AA | SEQ 731 | AA | SEQ 732 | AA | SEQ 733 | AA | SEQ 734 | AA | SEQ 735 | AA | SEQ 736 | AA | SEQ 737 | AA | SEQ 738 | AA | SEQ 739 | AA | SEQ 740 | AA | SEQ 741 | AA | SEQ 742 | AA | SEQ 743 | AA | SEQ 744 | AA | SEQ 745 | AA | SEQ 746 | AA | SEQ 747 | AA | SEQ 748 | AA | SEQ 749 | AA | SEQ 750 | AA | SEQ 751 | AA | SEQ 752 | AA | SEQ 753 | AA | SEQ 754 | AA | SEQ 755 | AA | SEQ 756 | AA | SEQ 757 | AA | SEQ 758 | AA | SEQ 759 | AA | SEQ 760 | AA | SEQ 761 | AA | SEQ 762 | AA | SEQ 763 | AA | SEQ 764 | AA | SEQ 765 | AA | SEQ 766 | AA | SEQ 767 | AA | SEQ 768 | AA | SEQ 769 | AA | SEQ 770 | AA | SEQ 771 | AA | SEQ 772 | AA | SEQ 773 | AA | SEQ 774 | AA | SEQ 775 | AA | SEQ 776 | AA | SEQ 777 | AA | SEQ 778 | AA | SEQ 779 | AA | SEQ 780 | AA | SEQ 781 | AA | SEQ 782 | AA | SEQ 783 | AA | SEQ 784 | AA | SEQ 785 | AA | SEQ 786 | AA | SEQ 787 | AA | SEQ 788 | AA | SEQ 789 | AA | SEQ 790 | AA | SEQ 791 | AA | SEQ 792 | AA | SEQ 793 | AA | SEQ 794 | AA | SEQ 795 | AA | SEQ 796 | AA | SEQ 797 | AA | SEQ 798 | AA | SEQ 799 | AA | SEQ 800 | AA | SEQ 801 | AA | SEQ 802 | AA | SEQ 803 | AA | SEQ 804 | AA | SEQ 805 | AA | SEQ 806 | AA | SEQ 807 | AA | SEQ 808 | AA | SEQ 809 | AA | SEQ 810 | AA | SEQ 811 | AA | SEQ 812 | AA | SEQ 813 | AA | SEQ 814 | AA | SEQ 815 | AA | SEQ 816 | AA | SEQ 817 | AA | SEQ 818 |
|-----------|-----------|------------|------------|-------------|--------|-------|-----|--------|------|----|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|
|-----------|-----------|------------|------------|-------------|--------|-------|-----|--------|------|----|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|--------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|----|---------|

Table 3 (cont'd)

| Name | Tumor sym | Normal sym | Tumor to | Tumor cells | Normal | Endos | p53 | SEQ 844 | TR5EO 43 | AA SEQ 47 | AA SEQ 48 | AA SEQ 49 | AA SEQ 51 | RA SEQ 52 | AA SEQ 54 | CD SEQ 55 | CI |
|-----------------------------|-----------|------------|----------|-------------|--------|-------|-----|---------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----|
| Hs 578T | 155 | | | | | | | 4159 | 0 | 64 | 0 | 1775 | 0 | 6701 | 15351 | 18395 | |
| MCF-7/ADR-RES | 151 | | | | | | | 3033 | 0 | 161 | 0 | 3752 | 0 | 1101 | 19471 | 4938 | |
| MCF7 | 149 | | | | | | | 0 | 0 | 1501 | 0 | 70511 | 0 | 16021 | 0 | 27225 | |
| Hs 578T | 149 | | | | | | | 0 | 0 | 0 | 0 | 5325 | 1681 | 5021 | 0 | 5025 | |
| UACC-257 | 147 | | | | | | | 0 | 0 | 47 | 45 | 3396 | 319 | 64 | 1253 | 4501 | |
| UACC-62 | 145 | | | | | | | 695 | 0 | 101 | 0 | 4290 | 195 | 221 | 0 | 5096 | |
| SK-MEL-26 | 144 | | | | | | | 604 | 0 | 0 | 0 | 5134 | 1814 | 426 | 0 | 6211 | |
| UO-31 | 143 | | | | | | | 755 | 0 | 14 | 0 | 4762 | 979 | 464 | 1913 | 6211 | |
| SK-MEL-5 | 142 | | | | | | | 1090 | 0 | 0 | 29 | 2880 | 299 | 437 | 368 | 1796 | |
| KM-12 | 141 | | | | | | | 0 | 0 | 4 | 0 | 2043 | 399 | 177 | 1507 | 18354 | |
| SK-MEL-2 | 140 | | | | | | | 0 | 0 | 0 | 0 | 6167 | 0 | 365 | 370 | 16901 | |
| HCT-116 | 139 | | | | | | | 1854 | 0 | 0 | 0 | 4947 | 25 | 311 | 10671 | 61770 | |
| SW-620 | 138 | | | | | | | 2152 | 0 | 222 | 339 | 5549 | 0 | 0 | 0 | 5225 | |
| COLO 205 | 137 | | | | | | | 6439 | 0 | 0 | 181 | 5635 | 0 | 0 | 0 | 11410 | |
| LOX IMVI | 136 | | | | | | | 1038 | 0 | 27 | 0 | 3694 | 1187 | 364 | 659 | 2486 | |
| SW-420 | 135 | | | | | | | 1665 | 0 | 0 | 10 | 3678 | 1663 | 344 | 905 | 11184 | |
| TK-10 | 134 | | | | | | | 519 | 0 | 107 | 104 | 3803 | 1066 | 193 | 0 | 8035 | |
| HCT-116 | 133 | | | | | | | 2701 | 0 | 7 | 110 | 3530 | 0 | 370 | 374 | 2945 | |
| 786-0 | 132 | | | | | | | 1371 | 0 | 0 | 63 | 6532 | 0 | 767 | 261 | 1701 | |
| HCC-T9806 | 131 | | | | | | | 0 | 0 | 0 | 104 | 4506 | 527 | 102 | 990 | 8637 | |
| ACHN | 130 | | | | | | | 0 | 0 | 0 | 0 | 3699 | 618 | 250 | 246 | 5609 | |
| PC-3 | 129 | | | | | | | 3345 | 0 | 11 | 212 | 3337 | 0 | 364 | 967 | 19597 | |
| RJF-393 | 128 | | | | | | | 455 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2441 | |
| QJA-145 | 127 | | | | | | | 0 | 0 | 132 | 160 | 4922 | 0 | 265 | 467 | 7704 | |
| C-641 | 126 | | | | | | | 1045 | 0 | 2 | 0 | 3578 | 0 | 0 | 0 | 7915 | |
| SR | 125 | | | | | | | 2368 | 0 | 126 | 305 | 4461 | 0 | 772 | 4011 | 12101 | |
| A498 | 124 | | | | | | | 0 | 0 | 0 | 3952 | 1414 | 102 | 647 | 5650 | | |
| HPM 8226 | 123 | | | | | | | 0 | 0 | 0 | 268 | 4346 | 1782 | 350 | 1146 | 10454 | |
| SH-2C | 122 | | | | | | | 0 | 0 | 144 | 3536 | 0 | 203 | 0 | 378 | 4657 | |
| Hs-60 | 121 | | | | | | | 591 | 0 | 24 | 0 | 3217 | 559 | 63 | 329 | 7486 | |
| MOLT-4 | 119 | | | | | | | 575 | 0 | 56 | 20 | 4528 | 0 | 85 | 4365 | 7866 | |
| OVCA1-5 | 118 | | | | | | | 0 | 0 | 0 | 0 | 7270 | 0 | 372 | 2107 | 2643 | |
| K-562 | 117 | | | | | | | 1705 | 0 | 0 | 0 | 8408 | 2352 | 307 | 4352 | 12624 | |
| OVCA1-4 | 116 | | | | | | | 518 | 0 | 70 | 0 | 3941 | 150 | 1813 | 852 | 14584 | |
| CCR6-CEM | 115 | | | | | | | 2335 | 0 | 56 | 0 | 3837 | 0 | 180 | 281 | 5529 | |
| OVCA1-3 | 114 | | | | | | | 841 | 0 | 21 | 0 | 3003 | 813 | 0 | 183 | 4097 | |
| SF-539 | 113 | | | | | | | 527 | 0 | 0 | 188 | 3830 | 206 | 25 | 911 | 14323 | |
| HOP-62 | 112 | | | | | | | 678 | 0 | 9 | 210 | 1431 | 2445 | 393 | 801 | 6165 | |
| SF-295 | 111 | | | | | | | 1174 | 0 | 0 | 183 | 6431 | 1777 | 654 | 1299 | 11830 | |
| ASBMA1CC | 110 | | | | | | | 863 | 0 | 0 | 112 | 2981 | 432 | 102 | 1093 | 5908 | |
| SF-268 | 109 | | | | | | | 0 | 0 | 21 | 0 | 5351 | 1071 | 403 | 331 | 7524 | |
| NCL-HS22 | 108 | | | | | | | 1587 | 0 | 0 | 474 | 4687 | 640 | 231 | 1215 | 5432 | |
| U251 | 107 | | | | | | | 254 | 0 | 221 | 41 | 4589 | 651 | 345 | 0 | 1015 | |
| NCL-H460 | 106 | | | | | | | 863 | 0 | 761 | 3 | 2867 | 833 | 300 | 0 | 8635 | |
| SMB-75 | 105 | | | | | | | 0 | 0 | 0 | 28 | 2980 | 134 | 348 | 0 | 4580 | |
| NCL-HS32M | 104 | | | | | | | 20 | 0 | 631 | 0 | 3171 | 1079 | 491 | 2068 | 4580 | |
| SMB-19 | 103 | | | | | | | 4486 | 0 | 19 | 0 | 7057 | 1691 | 244 | 1819 | 7164 | |
| NCL-HS26 | 102 | | | | | | | 942 | 0 | 59 | 0 | 3732 | 2018 | 625 | 0 | 11044 | |
| SK-COV-3 | 101 | | | | | | | 200 | 0 | 142 | 0 | 3780 | 1369 | 492 | 1760 | 4586 | |
| NCL-HS23 | 100 | | | | | | | 0 | 0 | 0 | 0 | 4198 | 1010 | 780 | 0 | 6847 | |
| IGROV1 | 99 | | | | | | | 783 | 0 | 14 | 187 | 3052 | 0 | 445 | 36 | 2451 | |
| ERVL | 98 | | | | | | | 0 | 0 | 72 | 285 | 3056 | 79 | 46 | 151 | 2451 | |
| OVCA1-8 | 97 | | | | | | | 0 | 0 | 0 | 109 | 3869 | 1247 | 54 | 445 | 4634 | |
| HOP-62 | 96 | | | | | | | 1168 | 0 | 123 | 0 | 0 | 0 | 0 | 0 | 7421 | |
| h. keratinocyte 3/21/92 #17 | 48 | | | | | | | 2238 | 0 | 112 | 0 | 4154 | 0 | 0 | 0 | 2214 | |
| h. keratinocyte 10/1/92 #17 | 47 | | | | | | | 1943 | 0 | 0 | 328 | 3112 | 734 | 278 | 0 | 3115 | |
| h. keratinocyte 2/25/92 #10 | 46 | | | | | | | 0 | 0 | 115 | 0 | 3362 | 7036 | 256 | 3115 | 3115 | |
| TCGP | 26 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| AS49-1 | wt | | | | | | | 487 | 48 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | |
| AS49-3 | wt | | | | | | | 317 | 955 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| AS49-4 | wt | | | | | | | 321 | 109 | 62 | 0 | 0 | 0 | 0 | 0 | 0 | |
| AS49-5 | wt | | | | | | | 0 | 238 | 48 | 0 | 0 | 0 | 0 | 0 | 0 | |
| AS49-7 | mutant | | | | | | | 5801 | 2138 | 285 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ERVL-1 | mutant | | | | | | | 2147 | 841 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ERVL-4 | mutant | | | | | | | 2865 | 0 | 480 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ERVL-3 | mutant | | | | | | | 1030 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ERVL-5 | wt | | | | | | | 0 | 162 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ERVL-7 | wt | | | | | | | 403 | 0 | 46 | 0 | 0 | 0 | 0 | 0 | 0 | |
| MCF-7-1 | wt | | | | | | | 3124 | 0 | 116 | 0 | 0 | 0 | 0 | 0 | 0 | |
| MCF-7-3 | wt | | | | | | | 150 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| MCF-7-4 | wt | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| MCF-7-5 | wt | | | | | | | 649 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| MCF-7-7 | mutant | | | | | | | 0 | 1818 | 135 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ADR-RES-1 | mutant | | | | | | | 30924 | 0 | 290 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ADR-RES-3 | mutant | | | | | | | 4157 | 279 | 109 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ADR-RES-4 | mutant | | | | | | | 635 | 572 | 64 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ADR-RES-5 | mutant | | | | | | | 748 | 361 | 11 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ADR-RES-7 | wt | | | | | | | 2518 | 51 | 178 | 0 | 0 | 0 | 0 | 0 | 0 | |
| WI 38-1 | wt | | | | | | | 1365 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| WI 38-3 | wt | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| WI 38-4 | wt | | | | | | | 3098 | 0 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | |
| WI 38-5 | wt | | | | | | | 812 | 0 | 43 | 0 | 0 | 0 | 0 | 0 | 0 | |
| WI 38-7 | wt | | | | | | | 0 | 395 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | |
| HeLa-1 | HPV E6 | | | | | | | 852 | 0 | 50 | 0 | 0 | 0 | 0 | 0 | 0 | |
| HeLa-3 | HPV E6 | | | | | | | 848 | 0 | 115 | 0 | 0 | 0 | 0 | 0 | 0 | |
| HeLa-4 | HPV E6 | | | | | | | 2647 | 766 | 172 | 0 | 0 | 0 | 0 | 0 | 0 | |
| HeLa-5 | HPV E6 | | | | | | | 429 | 550 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | |
| HeLa-7 | mutant | | | | | | | 0 | 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| H1299-1 | mutant | | | | | | | 1149 | 0 | 193 | 0 | 0 | 0 | 0 | 0 | 0 | |
| H1299-3 | mutant | | | | | | | 1155 | 0 | 36 | 0 | 0 | 0 | 0 | 0 | 0 | |
| H1299-4 | mutant | | | | | | | 819 | 63 | 106 | 0 | 0 | 0 | 0 | 0 | 0 | |
| H1299-5 | wt | | | | | | | 0 | 0 | 71 | 0 | 0 | 0 | 0 | 0 | 0 | |
| H1299-7 | wt | | | | | | | 751 | 361 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| AS49-2 | mutant | | | | | | | 21741 | 2630 | 206 | 0 | 0 | 0 | 0 | 0 | 0 | |
| ERVL-2 | wt | | | | | | | 649 | 0 | 206 | 0 | 0 | 0 | 0 | 0 | 0 | |
| HCT-116-1 | wt | | | | | | | 9208 | 967 | 430 | 0 | 0 | 0 | 0 | 0 | 0 | |
| HCT-116-2 | mutant | | | | | | | 407 | 255 | 55 | 0 | 0 | 0 | 0 | 0 | 0 | |
| HIT-29-2 | wt | | | | | | | 1107 | 261 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | |
| SF539-1 | wt | | | | | | | 523 | 262 | 71 | 0 | 0 | 0 | 0 | 0 | 0 | |
| SF539-2 | mutant | | | | | | | 8794 | 164 | 139 | 0 | 0 | 0 | 0 | 0 | 0 | |
| SF-768-1 | mutant | | | | | | | 11614 | 4311 | 265 | 0 | 0 | 0 | 0 | 0 | 0 | |
| SF-268-2 | wt | | | | | | | 2660 | 701 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| OVCA1-1 | mutant | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| OVCA1-2 | mutant | | | | | | | 705 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| OVCA1-5-1 | wt | | | | | | | 367 | 448 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| OVCA1-5-2 | wt | | | | | | | 2194 | 0 | 43 | 0 | 0 | 0 | | | | |

176
Table 3 (cont'd)

| Tissue | Tumor - ym | Normal - ym | Tumor - lo | Tumor cells | Normal | Endes | p31 | SEQ 36 AA | SEQ 37 | WSEQ 40 | AA SEQ 43 | NE SEQ 66 | CA SEQ 68 | HR SEQ 110 | RSEQ 73 | HR SEQ 78 | AA |
|-------------------------------|------------|-------------|------------|-------------|--------|-------|-----|-----------|--------|---------|-----------|-----------|-----------|------------|---------|-----------|----|
| C636.1 | | | | 166 | | | | 865 | 4675 | 157 | 1028 | 972 | 1529 | 1954 | 17285 | 29405 | |
| T86-0 | | | | 168 | | | | 531 | 9750 | 227 | 978 | 277 | 8891 | 5204 | 82551 | 45518 | |
| T47D | | | | 165 | | | | 5005 | 8516 | 0 | 1074 | 352 | 565 | 2901 | 19273 | 39931 | |
| Ren-3 | | | | 171 | | | | 0 | 1953 | 0 | 234 | 13 | 137 | 1787 | 135 | 37972 | |
| CRL 1441 RNA B/30 | | | | 181 | | | | 276 | 3104 | 0 | 24 | 0 | 0 | 10581 | 0 | 13079 | |
| T811 unselected + DPhase | | | | 183 | | | | 197 | 1800 | 0 | 65 | 0 | 0 | 843 | 230 | 14567 | |
| KB poly A* | | | | 194 | | | | 0 | 5094 | 0 | 108 | 0 | 149 | 1518 | 628 | 31810 | |
| HOS poly A* | | | | 196 | | | | 297 | 3283 | 8277 | 0 | 0 | 578 | 2815 | 868 | 52778 | |
| ACHN | | | | 198 | | | | 0 | 6593 | 0 | 358 | 0 | 1158 | 4907 | 145927 | 26142 | |
| UACC-62 | | | | 200 | | | | 1497 | 9993 | 0 | 212 | 0 | 475 | 2325 | 2675 | 17274 | |
| WCF-TADARIES | | | | 202 | | | | 185 | 2228 | 753 | 0 | 11 | 381 | 1444 | 2587 | 14607 | |
| UTOS (Mundy) poly A* | | | | 204 | | | | 0 | 7612 | 0 | 104 | 0 | 0 | 1028 | 617 | 9607 | |
| WISH (Collagen) poly A* | | | | 206 | | | | 150 | 0 | 0 | 94 | 189 | 831 | 579 | 725 | 11442 | |
| 5S8 mekaka mRNA | | | | 208 | | | | 0 | 18176 | 0 | 623 | 53 | 0 | 2367 | 2915 | 60563 | |
| COL131 RNA B2/08 | | | | 218 | | | | 219 | 1862 | 0 | 298 | 0 | 261 | 1447 | 815 | 73044 | |
| WJ-30 72h 0.5%FBS 24h 10% FBS | | | | 219 | | | | 271 | 3187 | 1190 | 0 | 34 | 403 | 2293 | 0 | 41474 | |
| CRL 1441 + TPA (24h) B/30 | | | | 220 | | | | 0 | 5582 | 0 | 31 | 633 | 0 | 1066 | 63 | 18180 | |
| Ren-1 | | | | 221 | | | | 2780 | 2513 | 0 | 61 | 0 | 453 | 2919 | 158 | 45266 | |
| Ren-2 | | | | 223 | | | | 705 | 2808 | 0 | 1154 | 0 | 302 | 2128 | 47 | 41277 | |
| Ren-4 | | | | 225 | | | | 521 | 4049 | 0 | 31 | 0 | 1303 | 2242 | 85 | 30345 | |
| HOP-57 | | | | 241 | | | | 0 | 2362 | 0 | 218 | 0 | 87 | 1773 | 1338 | 19084 | |
| MOL T-4 | | | | 242 | | | | 646 | 6364 | 762 | 493 | 481 | 2628 | 3182 | 39419 | 23972 | |
| ECV4 | | | | 243 | | | | 22 | 13083 | 0 | 328 | 73 | 2139 | 6462 | 109714 | 30253 | |
| HL 60 | | | | 244 | | | | 0 | 14211 | 886 | 23 | 431 | 2407 | 3687 | 11999 | 39367 | |
| NCLH-7 | | | | 245 | | | | 950 | 13057 | 572 | 2945 | 167 | 3423 | 3364 | 95598 | 46201 | |
| RPW1 B/26 | | | | 246 | | | | 0 | 1320 | 489 | 179 | 0 | 354 | 2272 | 18378 | 26669 | |
| ASW/ATCC | | | | 247 | | | | 89 | 3450 | 691 | 518 | 38 | 494 | 1921 | 2385 | 18013 | |
| SR | | | | 248 | | | | 0 | 1814 | 303 | 0 | 23 | 24 | 2897 | 16201 | 17287 | |
| OVCAR-3 | | | | 249 | | | | 0 | 7397 | 0 | 214 | 120 | 1028 | 2424 | 7704 | 20878 | |
| HCT-15 | | | | 250 | | | | 0 | 10765 | 599 | 1456 | 0 | 3538 | 4642 | 105630 | 27562 | |
| OVCAR-4 | | | | 251 | | | | 823 | 1294 | 1330 | 0 | 189 | 473 | 905 | 1481 | 7613 | |
| UO-31 | | | | 252 | | | | 372 | 3404 | 0 | 0 | 6 | 143 | 547 | 1109 | 6300 | |
| OVCAR-5 | | | | 253 | | | | 2585 | 9438 | 1611 | 625 | 52 | 1734 | 3348 | 12208 | 24504 | |
| SM12C | | | | 254 | | | | 0 | 51127 | 504 | 176 | 188 | 3335 | 2875 | 26805 | 16317 | |
| OVCAR-8 | | | | 255 | | | | 0 | 6508 | 688 | 213 | 0 | 1122 | 1359 | 35633 | 14140 | |
| OS B6/1 | | | | 256 | | | | 827 | 17296 | 405 | 688 | 0 | 5903 | 5283 | 30147 | 36549 | |
| IGROV1 | | | | 257 | | | | 1194 | 8352 | 758 | 716 | 68 | 2032 | 3644 | 28934 | 31704 | |
| SK-MEL-2 | | | | 258 | | | | 0 | 5305 | 0 | 19 | 0 | 0 | 963 | 4987 | 15816 | |
| SK-LOV3 | | | | 259 | | | | 65 | 3527 | 0 | 200 | 0 | 1050 | 3782 | 6318 | 17004 | |
| SK-MEL-5 | | | | 260 | | | | 135 | 3811 | 0 | 48 | 101 | 1148 | 281 | 13582 | | |
| SF-539 | | | | 261 | | | | 3832 | 12225 | 0 | 664 | 150 | 7673 | 5560 | 62729 | 51506 | |
| SK-MEL-28 | | | | 262 | | | | 0 | 7037 | 0 | 384 | 0 | 1713 | 1591 | 5611 | 34907 | |
| K-562 | | | | 263 | | | | 987 | 8200 | 1949 | 1685 | 29 | 9059 | 4576 | 195694 | 61739 | |
| UACC-257 | | | | 264 | | | | 0 | 6275 | 0 | 1456 | 0 | 1580 | 2365 | 3456 | 29295 | |
| M14 | | | | 265 | | | | 0 | 2639 | 0 | 0 | 214 | 804 | 616 | 1176 | 17725 | |
| MCF7 | | | | 267 | | | | 829 | 16845 | 820 | 965 | 604 | 4658 | 6019 | 79777 | 80630 | |
| MDA-MB-435 | | | | 269 | | | | 144 | 6376 | 477 | 543 | 0 | 968 | 1657 | 1148 | 24187 | |
| HT278 | | | | 270 | | | | 14 | 4483 | 0 | 0 | 0 | 891 | 2525 | 28 | 41301 | |
| MDA-N | | | | 271 | | | | 276 | 7065 | 0 | 354 | 92 | 1299 | 1638 | 5866 | 18906 | |
| Y79 poly A* | | | | 273 | | | | 0 | 8894 | 0 | 379 | 0 | 3785 | 6025 | 24954 | 77961 | |
| HOS poly A* | | | | 289 | | | | 0 | 20758 | 17443 | 371 | 236 | 6785 | 4275 | 30666 | 76961 | |
| HTB36 24h TPA RNA B/23 | | | | 290 | | | | 783 | 3861 | 0 | 728 | 0 | 228 | 1392 | 22 | 31917 | |
| HELA EXP Q31838 | | | | 313 | | | | 634 | 1812 | 0 | 247 | 0 | 1500 | 2048 | 4161 | 38714 | |
| HTB36 On RNA | | | | 322 | | | | 1461 | 24464 | 0 | 0 | 989 | 3512 | 8180 | 3044 | 81664 | |
| HT347 | | | | 323 | | | | 404 | 4560 | 0 | 0 | 0 | 2939 | 3484 | 15827 | 48041 | |
| 5S8 mekaka RNA | | | | 324 | | | | 1327 | 40573 | 0 | 68 | 742 | 990 | 4386 | 69608 | | |
| HCL4226 | | | | 336 | | | | 677 | 6101 | 721 | 345 | 0 | 1515 | 2111 | 2329 | 37119 | |
| HOP-62 | | | | 337 | | | | 0 | 15366 | 0 | 906 | 78 | 2808 | 1717 | 36496 | 21036 | |
| MDA-MB-231 | | | | 338 | | | | 135 | 85815 | 1217 | 5728 | 121 | 25352 | 1378 | 258035 | 103178 | |
| U251 | | | | 339 | | | | 135 | 80374 | 117 | 1825 | 362 | 78784 | 3368 | 202544 | 111922 | |
| FT Cells poly A* | | | | 340 | | | | 483 | 1482 | 0 | 467 | 0 | 1987 | 2005 | 45862 | 16256 | |
| PC-3 | | | | 341 | | | | 177 | 13879 | 62 | 362 | 2730 | 5703 | 8884 | 40554 | 71885 | |
| HCC-2998 | | | | 343 | | | | 92 | 8206 | 0 | 552 | 369 | 1782 | 2288 | 23873 | 21578 | |
| SW-620 | | | | 345 | | | | 29 | 7776 | 0 | 621 | 209 | 1201 | 2041 | 10731 | 24715 | |
| HT192 | | | | 346 | | | | 1001 | 7290 | 408 | 182 | 0 | 1412 | 5254 | 2082 | 65823 | |
| COLO 205 | | | | 347 | | | | 162 | 9047 | 0 | 306 | 0 | 0 | 685 | 1304 | 8915 | |
| HT218 | | | | 348 | | | | 440 | 4819 | 0 | 72 | 158 | 0 | 1385 | 291 | 36889 | |
| NSA-12 | | | | 349 | | | | 49 | 11052 | 0 | 406 | 0 | 891 | 1119 | 34049 | 17488 | |
| HT151 | | | | 350 | | | | 138 | 6054 | 0 | 0 | 0 | 723 | 3737 | 4971 | 45600 | |
| A498 | | | | 351 | | | | 797 | 20305 | 0 | 401 | 1964 | 1038 | 2649 | 4743 | 30375 | |
| HT300 | | | | 352 | | | | 726 | 15335 | 57 | 0 | 0 | 2027 | 4435 | 5637 | 60935 | |
| EXP 393 | | | | 353 | | | | 153 | 8672 | 0 | 114 | 348 | 348 | 7229 | 2729 | 7430 | |
| TK-10 | | | | 355 | | | | 738 | 78660 | 694 | 3780 | 1673 | 23029 | 12524 | 129790 | 71952 | |
| Melano-34 | | | | 357 | | | | 2111 | 93276 | 13897 | 36786 | 2444 | 55479 | 34972 | 201421 | 150800 | |
| He S187 | | | | 359 | | | | 0 | 9184 | 0 | 88 | 82 | 2391 | 2875 | 6581 | 48992 | |
| HT13 | | | | 50 | | | | 0 | 8740 | 47 | 0 | 878 | 1707 | 0 | 52671 | | |
| HT288 | | | | 52 | | | | 179 | 8067 | 0 | 0 | 272 | 783 | 2581 | 7541 | 84143 | |
| HT139 | | | | 54 | | | | 921 | 8243 | 0 | 4 | 635 | 0 | 1926 | 276 | 65037 | |
| HT155 | | | | 56 | | | | 0 | 6690 | 0 | 281 | 632 | 2384 | 2131 | 2121 | 61017 | |
| HT163 | | | | 58 | | | | 10824 | 1302 | 364 | 25 | 281 | 1598 | 540 | 2415 | | |
| HT170 | | | | 60 | | | | 37 | 15071 | 0 | 252 | 0 | 1662 | 4224 | 15427 | 83039 | |
| HT172 | | | | 62 | | | | 0 | 3376 | 0 | 0 | 17 | 284 | 875 | 0 | 46245 | |
| HT138 | | | | 63 | | | | 0 | 2623 | 0 | 0 | 43 | 767 | 1070 | 4034 | 45691 | |
| HT178 | | | | 64 | | | | 31 | 31995 | 0 | 0 | 145 | 349 | 974 | 609 | 51923 | |
| HT154 | | | | 65 | | | | 0 | 1277 | 2364 | 0 | 44 | 108 | 1138 | 0 | 52719 | |
| HT180 | | | | 66 | | | | 276 | 2597 | 0 | 58 | 0 | 862 | 865 | 197 | 43129 | |
| HT169 | | | | 68 | | | | 427 | 4840 | 0 | 0 | 229 | 209 | 455 | 1239 | 26590 | |
| HT180 | | | | 68 | | | | 69 | 4083 | 286 | 122 | 0 | 346 | 1043 | 3365 | 78481 | |
| HT143 | | | | 69 | | | | 2067 | 248 | 0 | 0 | 161 | 628 | 42 | 38405 | | |
| HT190 | | | | 70 | | | | 0 | 5719 | 954 | 58 | 0 | 0 | 1854 | 0 | 59909 | |
| HT145 | | | | 71 | | | | 1053 | 3301 | 539 | 0 | 74 | 3282 | 1633 | 230 | 56887 | |
| HT227 | | | | 72 | | | | 0 | 6795 | 0 | 83 | 183 | 2496 | 1828 | 277 | 65548 | |
| HT202 | | | | 73 | | | | 0 | 18128 | 0 | 439 | 112 | 0 | 2601 | 865 | 84661 | |
| HT214 | | | | 74 | | | | 0 | 10943 | 138 | 0 | 41 | 279 | 1755 | 1196 | 51097 | |
| HT217 | | | | 76 | | | | 275 | 25792 | 0 | 2002 | 651 | 86 | 5151 | 5403 | 100831 | |
| HeLa fibroblasts B425 11/8 | | | | 77 | | | | 0 | 3161 | 0 | 126 | 250 | 0 | 3011 | 615 | 39514 | |

177
Table 3 (cont'd)

178
Table 3 (cont'd)

| Tissue | Tumor sym | Normal sym | Tumor, to | Tumor cells | Normal | Endos | p53 | SEQ 36 | AA | SEQ 37 | WT | SEQ 60 | AA | SEQ 63 | NE | SEQ 66 | CA | SEQ 68 | HR | SEQ 118 | R | SEQ 73 | HR | SEQ 78 | AA |
|------------------------|-----------|------------|-----------|-------------|--------|-------|--------|--------|-------|--------|--------|--------|-------|--------|-------|--------|----|--------|----|---------|---|--------|----|--------|----|
| DaFang-7 | | | | | | | | 0 | 50728 | 3124 | 2203 | 0 | 2725 | 1021 | 10539 | 11048 | | | | | | | | | |
| DaFang-8 | | | | | | | | 0 | 35361 | 84 | 3207 | 0 | 2819 | 569 | 23676 | 14951 | | | | | | | | | |
| DaFang-9 | | | | | | | | 0 | 28319 | 0 | 4298 | 0 | 4247 | 714 | 52151 | 12734 | | | | | | | | | |
| DaFang-11 | | | | | | | | 0 | 40638 | 0 | 6022 | 0 | 3724 | 1086 | 45305 | 13175 | | | | | | | | | |
| DaFang-12 | | | | | | | | 0 | 16274 | 0 | 1652 | 0 | 2814 | 832 | 58583 | 11807 | | | | | | | | | |
| DaFang-10 | | | | | | | | 0 | 18015 | 0 | 1365 | 0 | 42701 | 801 | 34052 | 11401 | | | | | | | | | |
| DaFang-1 | | | | | | | | 0 | 11739 | 0 | 214431 | 0 | 2078 | 1021 | 20203 | 22794 | | | | | | | | | |
| DaFang-2 | | | | | | | | 0 | 9371 | 0 | 13705 | 0 | 1538 | 783 | 15252 | 16156 | | | | | | | | | |
| DaFang-3 | | | | | | | | 0 | 6905 | 1171 | 95151 | 0 | 503 | 923 | 31807 | 25569 | | | | | | | | | |
| DaFang-4 | | | | | | | | 0 | 4899 | 0 | 510 | 0 | 1746 | 690 | 20143 | 25155 | | | | | | | | | |
| DaFang-5 | | | | | | | | 0 | 3723 | 0 | 716 | 0 | 1018 | 548 | 9931 | 12544 | | | | | | | | | |
| DaFang-6 | | | | | | | | 0 | 39944 | 0 | 0 | 0 | 465 | 482 | 1925 | 9565 | | | | | | | | | |
| AS49-8 | | | | | | | wt | 0 | 4018 | 537 | 1675 | 0 | 2260 | 398 | 19015 | 13633 | | | | | | | | | |
| EXVX-8 | | | | | | | mutant | 0 | 6749 | 0 | 5081 | 0 | 4361 | 801 | 24268 | 14160 | | | | | | | | | |
| HCT-116-7 | | | | | | | wt | 0 | 2845 | 597 | 89 | 0 | 812 | 478 | 8413 | 12883 | | | | | | | | | |
| HCT-116-8 | | | | | | | wt | 0 | 5165 | 3418 | 899 | 0 | 302 | 391 | 11432 | 18508 | | | | | | | | | |
| HT29-1 | | | | | | | mutant | 0 | 2474 | 0 | 1963 | 0 | 1494 | 451 | 25516 | 21737 | | | | | | | | | |
| HT29-2 | | | | | | | mutant | 0 | 1053 | 0 | 54 | 0 | 307 | 209 | 9185 | 13162 | | | | | | | | | |
| HT29-3 | | | | | | | mutant | 0 | 4333 | 0 | 2962 | 0 | 709 | 594 | 16207 | 19784 | | | | | | | | | |
| SF539-7 | | | | | | | wt | 0 | 8603 | 29 | 866 | 0 | 1074 | 1086 | 12408 | 17808 | | | | | | | | | |
| SF539-8 | | | | | | | wt | 0 | 8996 | 0 | 150 | 0 | 856 | 911 | 14376 | 16098 | | | | | | | | | |
| SF-268-7 | | | | | | | mutant | 0 | 6810 | 1896 | 708 | 0 | 1316 | 420 | 14248 | 15443 | | | | | | | | | |
| SF-268-8 | | | | | | | mutant | 0 | 9705 | 0 | 1894 | 0 | 2052 | 568 | 12101 | 14424 | | | | | | | | | |
| OVCAR-4-7 | | | | | | | wt | 0 | 1789 | 0 | 507 | 0 | 501 | 100 | 3378 | 14756 | | | | | | | | | |
| OVCAR-4-8 | | | | | | | wt | 0 | 8000 | 789 | 12121 | 0 | 3077 | 730 | 17308 | 16046 | | | | | | | | | |
| OVCAR-5-7 | | | | | | | mutant | 0 | 6291 | 0 | 1758 | 0 | 18 | 1330 | 20088 | 37871 | | | | | | | | | |
| OVCAR-5-8 | | | | | | | mutant | 0 | 3819 | 11046 | 46 | 0 | 2526 | 289 | 8074 | 10551 | | | | | | | | | |
| MCF-7-8 | | | | | | | wt | 0 | 4047 | 348 | 1398 | 0 | 543 | 451 | 15697 | 63544 | | | | | | | | | |
| ADR-RES-8 | | | | | | | mutant | 0 | 4033 | 485 | 2093 | 0 | 479 | 92 | 19755 | 12562 | | | | | | | | | |
| HuLa-8 | | | | | | | wt | 0 | 4132 | 814 | 1078 | 0 | 1073 | 705 | 11463 | 19305 | | | | | | | | | |
| SW480-7 | | | | | | | mutant | 0 | 3841 | 555 | 846 | 0 | 1028 | 212 | 13765 | 11456 | | | | | | | | | |
| SW480-8 | | | | | | | mutant | 0 | 3095 | 0 | 1133 | 0 | 215 | 450 | 3673 | 6636 | | | | | | | | | |
| HT29-8 | | | | | | | mutant | 0 | 8441 | 8774 | 1442 | 0 | 987 | 460 | 8507 | 12969 | | | | | | | | | |
| C3A-7 | | | | | | | mutant | 0 | 6455 | 0 | 131 | 0 | 934 | 331 | 1068 | 11745 | | | | | | | | | |
| C3A-8 | | | | | | | mutant | 0 | 4384 | 0 | 456 | 0 | 1860 | 1422 | 9025 | 25099 | | | | | | | | | |
| UZOS-7 | | | | | | | mutant | 0 | 5403 | 395 | 0 | 0 | 1824 | 251 | 21545 | 17515 | | | | | | | | | |
| UZOS-8 | | | | | | | mutant | 0 | 4223 | 1977 | 1921 | 0 | 2486 | 614 | 32498 | 11293 | | | | | | | | | |
| HuLa-7 | | | | | | | wt | 0 | 4735 | 17844 | 462 | 0 | 888 | 614 | 10835 | 18314 | | | | | | | | | |
| HuLa-8 | | | | | | | wt | 0 | 4538 | 0 | 1181 | 0 | 573 | 583 | 35697 | 17704 | | | | | | | | | |
| WI 38-8 | | | | | | | wt | 0 | 8860 | 0 | 0 | 0 | 2756 | 893 | 1133 | 17515 | | | | | | | | | |
| 458 medulla RNA | | | | | | | wt | 219 | 16478 | 0 | 4697 | 322 | 11543 | 2288 | 4332 | 123911 | | | | | | | | | |
| CR15/2 3/17/89 | | | | | | | wt | 0 | 1425 | 79 | 288 | 0 | 0 | 1482 | 969 | 33047 | | | | | | | | | |
| Bep-4 | | | | | | | wt | 1359 | 7179 | 0 | 471 | 66 | 4171 | 2041 | 13126 | 60734 | | | | | | | | | |
| HT368 | | | | | | | wt | 415 | 10978 | 366 | 132 | 228 | 1211 | 1604 | 51273 | 6636 | | | | | | | | | |
| HT378 | | | | | | | wt | 394 | 1670 | 0 | 43 | 0 | 970 | 1344 | 481 | 84588 | | | | | | | | | |
| HT385 | | | | | | | wt | 2684 | 23718 | 1052 | 187 | 825 | 1605 | 3482 | 3271 | 115925 | | | | | | | | | |
| HT308 | | | | | | | wt | 494 | 4362 | 0 | 0 | 167 | 1896 | 2614 | 7469 | 23383 | | | | | | | | | |
| Bep-3 | | | | | | | 173 | 142 | 2903 | 0 | 68 | 0 | 1453 | 2663 | 25133 | 47794 | | | | | | | | | |
| Bep-5 | | | | | | | 175 | 1326 | 807 | 0 | 54 | 0 | 832 | 1043 | 678 | 27812 | | | | | | | | | |
| Bep-9 | | | | | | | 177 | 0 | 1932 | 516 | 109 | 0 | 315 | 1821 | 763 | 37803 | | | | | | | | | |
| h her2/neu 2/25/92 #10 | | | | | | | 237 | 1100 | 3331 | 611 | 85 | 878 | 1031 | 1884 | 280 | 44367 | | | | | | | | | |
| HTB10 | | | | | | | wt | 0 | 6858 | 266 | 827 | 0 | 504 | 5317 | 197 | 84103 | | | | | | | | | |
| h her2/neu 3/31/92 #12 | | | | | | | wt | 165 | 4732 | 0 | 30 | 9 | 1643 | 2487 | 119 | 63251 | | | | | | | | | |
| prostate h | | | | | | | wt | 97 | 709 | 66 | 151 | 47 | 840 | 1629 | 0 | 71260 | | | | | | | | | |
| h hMG-OS poly A+ | | | | | | | wt | 0 | 9770 | 1806 | 300 | 186 | 2527 | 2510 | 834 | 6636 | | | | | | | | | |
| SA-OS (hMG-OS) poly A+ | | | | | | | wt | 588 | 31235 | 0 | 101 | 1671 | 2813 | 28633 | 3973 | 62966 | | | | | | | | | |
| MAK poly A+ | | | | | | | wt | 272 | 28963 | 0 | 36 | 1131 | 4200 | 3944 | 5141 | 46333 | | | | | | | | | |
| HCT-116-3 | | | | | | | wt | 0 | 2264 | 530 | 2001 | 0 | 506 | 457 | 6561 | 14135 | | | | | | | | | |
| HCT-116-4 | | | | | | | wt | 0 | 3670 | 171 | 639 | 0 | 388 | 241 | 16248 | 16344 | | | | | | | | | |
| HCT-116-5 | | | | | | | wt | 0 | 8838 | 209 | 224 | 0 | 477 | 389 | 13553 | 16473 | | | | | | | | | |
| HCT-116-6 | | | | | | | wt | 0 | 5156 | 1378 | 2077 | 0 | 263 | 483 | 11650 | 12955 | | | | | | | | | |
| AS49-6 | | | | | | | wt | 0 | 777 | 0 | 42 | 0 | 899 | 315 | 2191 | 14864 | | | | | | | | | |
| HT29-3 | | | | | | | mutant | 0 | 3211 | 1117 | 2356 | 0 | 1884 | 511 | 14621 | 15623 | | | | | | | | | |
| EXVX-6 | | | | | | | mutant | 0 | 919 | 80 | 0 | 0 | 367 | 636 | 9049 | 16148 | | | | | | | | | |
| HT29-4 | | | | | | | mutant | 0 | 771 | 1454 | 875 | 0 | 899 | 409 | 13595 | 21159 | | | | | | | | | |
| HT29-5 | | | | | | | mutant | 0 | 3498 | 1303 | 4091 | 0 | 1303 | 1063 | 25245 | 27154 | | | | | | | | | |
| HT29-6 | | | | | | | mutant | 0 | 3158 | 113 | 3054 | 0 | 1090 | 524 | 29241 | 30150 | | | | | | | | | |
| OVCAR-4-3 | | | | | | | wt | 0 | 869 | 1624 | 4736 | 0 | 764 | 229 | 81071 | 12950 | | | | | | | | | |
| OVCAR-4-4 | | | | | | | wt | 0 | 3487 | 0 | 1105 | 0 | 385 | 68 | 11844 | 11168 | | | | | | | | | |
| OVCAR-4-5 | | | | | | | wt | 0 | 12920 | 1901 | 4206 | 0 | 807 | 375 | 86133 | 14195 | | | | | | | | | |
| OVCAR-4-6 | | | | | | | wt | 0 | 3670 | 1385 | 0 | 0 | 1030 | 64 | 20409 | 15154 | | | | | | | | | |
| SF539-3 | | | | | | | wt | 0 | 8954 | 177 | 706 | 0 | 920 | 168 | 8632 | 15264 | | | | | | | | | |
| SF539-4 | | | | | | | wt | 0 | 11231 | 435 | 204 | 0 | 413 | 194 | 14684 | 10033 | | | | | | | | | |
| SF539-5 | | | | | | | wt | 0 | 12548 | 396 | 469 | 0 | 642 | 352 | 4084 | 13777 | | | | | | | | | |
| SF539-6 | | | | | | | wt | 0 | 5156 | 0 | 0 | 0 | 2221 | 362 | 14533 | 20181 | | | | | | | | | |
| OVCAR-5-3 | | | | | | | mutant | 0 | 4326 | 296 | 1341 | 0 | 1507 | 21 | 8827 | 14804 | | | | | | | | | |
| OVCAR-5-4 | | | | | | | mutant | 0 | 3508 | 0 | 1061 | 0 | 848 | 488 | 8731 | 13868 | | | | | | | | | |
| OVCAR-5-5 | | | | | | | mutant | 0 | 2838 | 0 | 69 | 0 | 766 | | | | | | | | | | | | |

179
Table 3 (cont'd)

[illegible]

181
Table 3 (cont'd)

| Tissue | Tumor-adj | Normal-adj | Tumor-to | Tumor cells | normal | Endo | p53 | SEQ 79 AA | SEQ 80 AA | SEQ 81 AA | SEQ 82 AA | SEQ 83 AA | SEQ 84 AA | SEQ 85 AA | SEQ 86 AA | SEQ 87 AA | SEQ 88 AA | SEQ 89 AA | SEQ 90 AA | SEQ 91 AA | SEQ 92 AA | SEQ 93 AA | SEQ 94 AA | |
|-----------------------|-----------|------------|----------|-------------|--------|------|-----|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|--|
| HA 5721 | 155 | | | | | | | 275 | 156 | 133245 | 4602 | 2616031 | 30771 | 326 | 831 | 3393 | | | | | | | | |
| MCF-TADR-RES | 151 | | | | | | | 454 | 0 | 62589 | 3763 | 173587 | 840 | 234 | 71 | 4602 | | | | | | | | |
| MCF7 | 149 | | | | | | | 0 | 98 | 22491 | 3843 | 219251 | 40 | 463 | 50 | 4216 | | | | | | | | |
| M14 | 147 | | | | | | | 34 | 0 | 102635 | 5796 | 68626 | 134 | 4631 | 18 | 8105 | | | | | | | | |
| UACC-257 | 145 | | | | | | | 0 | 190 | 44964 | 4458 | 46556 | 1177 | 177 | 77 | 5052 | | | | | | | | |
| UACC-26 | 144 | | | | | | | 0 | 331 | 105560 | 8515 | 47918 | 1123 | 348 | 0 | 8145 | | | | | | | | |
| SK-MEL-2 | 143 | | | | | | | 0 | 103 | 35141 | 6515 | 65339 | 575 | 133 | 24 | 1529 | | | | | | | | |
| UO-31 | 142 | | | | | | | 508 | 100 | 20643 | 9249 | 73214 | 520 | 189 | 275 | 79 | | | | | | | | |
| SK-MEL-5 | 141 | | | | | | | 104 | 0 | 29587 | 6756 | 73371 | 1055 | 79 | 11 | 2500 | | | | | | | | |
| RM-12 | 140 | | | | | | | 416 | 0 | 3454 | 3354 | 80653 | 109 | 127 | 182 | 3169 | | | | | | | | |
| SK-MEL-2 | 139 | | | | | | | 171 | 0 | 22819 | 3246 | 134929 | 27 | 167 | 132 | 2782 | | | | | | | | |
| HCT-15 | 138 | | | | | | | 0 | 47 | 15092 | 3913 | 104930 | 599 | 0 | 1031 | 7894 | | | | | | | | |
| Melan-34 | 137 | | | | | | | 148 | 150 | 22468 | 5765 | 137583 | 977 | 279 | 0 | 3750 | | | | | | | | |
| COLO 205 | 136 | | | | | | | 0 | 213 | 21011 | 5643 | 144441 | 642 | 91 | 74 | 5493 | | | | | | | | |
| LOX IMV | 135 | | | | | | | 156 | 1464 | 58997 | 3350 | 112245 | 1470 | 0 | 0 | 2197 | | | | | | | | |
| SW 620 | 134 | | | | | | | 166 | 0 | 11595 | 3617 | 104047 | 788 | 0 | 210 | 6215 | | | | | | | | |
| TK-10 | 133 | | | | | | | 0 | 137 | 23867 | 4146 | 75724 | 1065 | 130 | 0 | 4536 | | | | | | | | |
| HCT 116 | 132 | | | | | | | 1060 | 59 | 74651 | 2016 | 119724 | 702 | 83 | 263 | 7449 | | | | | | | | |
| T86-0 | 131 | | | | | | | 225 | 0 | 26315 | 3039 | 102477 | 3314 | 0 | 42 | 6256 | | | | | | | | |
| HCC-T208 | 130 | | | | | | | 0 | 190 | 17067 | 5568 | 127191 | 455 | 16 | 0 | 9023 | | | | | | | | |
| AGHN | 129 | | | | | | | 0 | 138 | 35733 | 4255 | 87608 | 473 | 165 | 144 | 2392 | | | | | | | | |
| PC-3 | 128 | | | | | | | 160 | 104 | 8373 | 2715 | 80475 | 1017 | 248 | 0 | 7409 | | | | | | | | |
| DU145 | 127 | | | | | | | 134 | 204 | 35080 | 3502 | 59563 | 377 | 298 | 65 | 7546 | | | | | | | | |
| Caki-1 | 126 | | | | | | | 0 | 79 | 6334 | 2431 | 17433 | 259 | 54 | 0 | 2817 | | | | | | | | |
| SR | 125 | | | | | | | 0 | 141 | 62167 | 2648 | 84362 | 3136 | 0 | 0 | 5203 | | | | | | | | |
| AJBR | 124 | | | | | | | 0 | 79 | 8485 | 2584 | 28629 | 360 | 47 | 10019 | 0 | | | | | | | | |
| RPMB 8226 | 123 | | | | | | | 0 | 153 | 26455 | 2600 | 91356 | 15 | 1182 | 0 | 6992 | | | | | | | | |
| SM12C | 122 | | | | | | | 0 | 24 | 0 | 80 | 2614 | 12634 | 473 | 168 | 4326 | | | | | | | | |
| HL 60 | 121 | | | | | | | 0 | 0 | 35753 | 7382 | 36641 | 542 | 522 | 84 | 11656 | | | | | | | | |
| MEL-T-4 | 120 | | | | | | | 613 | 109 | 925 | 8301 | 450 | 369 | 314 | 173 | 21430 | | | | | | | | |
| OVCA-5 | 119 | | | | | | | 0 | 0 | 909 | 5372 | 83742 | 4346 | 27 | 0 | 3065 | | | | | | | | |
| K-562 | 118 | | | | | | | 425 | 0 | 620 | 4872 | 41219 | 4813 | 1262 | 10 | 4433 | | | | | | | | |
| OVCA-4 | 117 | | | | | | | 258 | 0 | 10918 | 4092 | 106477 | 259 | 97 | 70 | 6579 | | | | | | | | |
| CCRF-CEM | 116 | | | | | | | 654 | 246 | 21540 | 2514 | 133148 | 8057 | 231 | 0 | 3791 | | | | | | | | |
| OVCA-3 | 115 | | | | | | | 0 | 0 | 16299 | 3482 | 113784 | 6977 | 144 | 0 | 5240 | | | | | | | | |
| CCRF-CEM | 114 | | | | | | | 464 | 37 | 13067 | 2665 | 95833 | 1365 | 33 | 0 | 3461 | | | | | | | | |
| OVCA-3 | 113 | | | | | | | 247 | 0 | 14169 | 3862 | 95278 | 2343 | 119 | 0 | 5506 | | | | | | | | |
| SF-539 | 112 | | | | | | | 404 | 153 | 35836 | 1330 | 72109 | 2689 | 0 | 0 | 5448 | | | | | | | | |
| HOP-62 | 111 | | | | | | | 281 | 6 | 21130 | 3579 | 98198 | 3313 | 0 | 5 | 13804 | | | | | | | | |
| SF-295 | 110 | | | | | | | 1005 | 321 | 44866 | 4014 | 130106 | 3808 | 220 | 0 | 4485 | | | | | | | | |
| AS54WATCC | 109 | | | | | | | 0 | 2917 | 0 | 2917 | 136766 | 900 | 446 | 416 | 2028 | | | | | | | | |
| SF-268 | 108 | | | | | | | 364 | 213 | 33088 | 7465 | 81136 | 3557 | 225 | 113 | 4126 | | | | | | | | |
| NCLH522 | 107 | | | | | | | 292 | 0 | 24593 | 5009 | 148017 | 1964 | 183 | 253 | 7311 | | | | | | | | |
| U251 | 106 | | | | | | | 170 | 216 | 27031 | 2699 | 48575 | 3614 | 21 | 0 | 4382 | | | | | | | | |
| NCLH460 | 105 | | | | | | | 166 | 335 | 5667 | 1862 | 66812 | 143 | 0 | 0 | 8291 | | | | | | | | |
| SNB-75 | 104 | | | | | | | 212 | 0 | 23147 | 4126 | 72618 | 1194 | 0 | 0 | 5616 | | | | | | | | |
| NCLH322M | 103 | | | | | | | 139 | 58 | 6406 | 2982 | 17270 | 1903 | 0 | 87 | 6176 | | | | | | | | |
| SNB-19 | 102 | | | | | | | 211 | 119 | 21514 | 5630 | 11321 | 4083 | 0 | 298 | 10900 | | | | | | | | |
| NCLH225 | 101 | | | | | | | 0 | 0 | 5634 | 7381 | 19830 | 5644 | 272 | 171 | 3861 | | | | | | | | |
| SK-OV-3 | 100 | | | | | | | 319 | 432 | 61716 | 2994 | 2378 | 1016 | 187 | 64 | 9311 | | | | | | | | |
| NCLH23 | 99 | | | | | | | 0 | 282 | 6156 | 2107 | 15131 | 1772 | 413 | 2151 | 12724 | | | | | | | | |
| UICR01 | 98 | | | | | | | 62 | 132 | 28193 | 4584 | 5729 | 613 | 373 | 0 | 4466 | | | | | | | | |
| ERVK1 | 97 | | | | | | | 106 | 23 | 5309 | 5309 | 2072 | 116 | 0 | 0 | 8109 | | | | | | | | |
| OVCA-8 | 96 | | | | | | | 0 | 254 | 18997 | 7191 | 3604 | 15079 | 305 | 0 | 12100 | | | | | | | | |
| HOP-92 | 95 | | | | | | | 315 | 260 | 22446 | 6764 | 150645 | 4899 | 414 | 0 | 4885 | | | | | | | | |
| h keratins 3/1/92 #12 | 94 | | | | | | | 0 | 0 | 1800 | 7249 | 12385 | 634 | 456 | 284 | 4382 | | | | | | | | |
| h keratins 3/1/92 #17 | 47 | | | | | | | 0 | 0 | 13009 | 9192 | 188015 | 116 | 117 | 0 | 5760 | | | | | | | | |
| h keratins 3/1/92 #10 | 46 | | | | | | | 0 | 16 | 11006 | 6235 | 81465 | 341 | 226 | 0 | 14132 | | | | | | | | |
| TCGP | 26 | | | | | | | wt | 0 | 49 | 3553 | 63185 | 0 | 3072 | 0 | 48 | 110 | | | | | | | |
| AS49-1 | | | | | | | | wt | 0 | 22 | 0 | 46138 | 0 | 0 | 0 | 276 | 998 | | | | | | | |
| AS49-3 | | | | | | | | wt | 0 | 62 | 118 | 46247 | 0 | 1843 | 0 | 342 | 754 | | | | | | | |
| AS49-4 | | | | | | | | wt | 0 | 306 | 2509 | 72567 | 0 | 2142 | 0 | 0 | 1102 | | | | | | | |
| AS49-5 | | | | | | | | wt | 0 | 58 | 831 | 39860 | 0 | 889 | 0 | 0 | 1377 | | | | | | | |
| AS49-7 | | | | | | | | mutant | 0 | 296 | 2606 | 66834 | 0 | 1755 | 0 | 130 | 130 | | | | | | | |
| ERVK-1 | | | | | | | | mutant | 0 | 223 | 714 | 150881 | 0 | 10601 | 0 | 126 | 1699 | | | | | | | |
| ERVK-4 | | | | | | | | mutant | 0 | 359 | 49 | 77798 | 0 | 6784 | 0 | 0 | 824 | | | | | | | |
| ERVK-3 | | | | | | | | mutant | 0 | 16 | 1208 | 37631 | 0 | 898 | 0 | 187 | 2202 | | | | | | | |
| ERVK-5 | | | | | | | | wt | 0 | 1153 | 80 | 74369 | 0 | 703 | 0 | 0 | 4466 | | | | | | | |
| ERVK-7 | | | | | | | | wt | 0 | 550 | 0 | 41681 | 0 | 322 | 0 | 0 | 1185 | | | | | | | |
| MCF-7-1 | | | | | | | | wt | 0 | 234 | 0 | 37645 | 0 | 0 | 0 | 124 | 574 | | | | | | | |
| MCF-7-3 | | | | | | | | wt | 0 | 182 | 1025 | 32082 | 0 | 648 | 0 | 91 | 561 | | | | | | | |
| MCF-7-4 | | | | | | | | wt | 0 | 0 | 0 | 25975 | 0 | 880 | 0 | 429 | 4630 | | | | | | | |
| MCF-7-5 | | | | | | | | wt | 0 | 264 | 20 | 21865 | 0 | 0 | 0 | 0 | 697 | | | | | | | |
| MCF-7-7 | | | | | | | | mutant | 0 | 744 | 1610 | 89435 | 0 | 2747 | 0 | 912 | 1775 | | | | | | | |
| ADR-RES-1 | | | | | | | | mutant | 0 | 911 | 2497 | 43852 | 0 | 860 | 0 | 175 | 1127 | | | | | | | |
| ADR-RES-3 | | | | | | | | mutant | 0 | 445 | 218 | 40637 | 0 | 1142 | 0 | 73 | 1422 | | | | | | | |
| ADR-RES-4 | | | | | | | | wt | 0 | 253 | 1236 | 85684 | 0 | 1779 | 0 | 231 | 248 | | | | | | | |
| ADR-RES-5 | | | | | | | | mutant | 0 | 473 | 4304 | 27945 | 0 | 1085 | 0 | 0 | 924 | | | | | | | |
| ADR-RES-7 | | | | | | | | wt | 0 | 953 | 3084 | 67921 | 0 | 19059 | 0 | 110 | 2042 | | | | | | | |
| WI 38-1 | | | | | | | | | | | | | | | | | | | | | | | | |

182
Table 3 (cont'd)

| Tissue | Tumor sym | Normal sym | Tumor - to | Tumor cells | Normal | Endos | p53 | SEQ 79 | AA | SEQ 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 |
|-----------------------------|-----------|------------|------------|-------------|--------|-------|--------|--------|-------|--------|--------|--------|-------|------|------|-------|------|----|----|----|----|----|----|----|----|
| DaPeng-1 | | | | | | | | 0 | 11671 | 22871 | 940671 | 0 | 7232 | 0 | 228 | 0 | 1229 | | | | | | | | |
| DaPeng-2 | | | | | | | | 0 | 2156 | 83 | 72285 | 0 | 8513 | 0 | 48 | 0 | 671 | | | | | | | | |
| DaPeng-3 | | | | | | | | 0 | 2323 | 15 | 36655 | 0 | 14281 | 0 | 103 | 0 | 750 | | | | | | | | |
| DaPeng-11 | | | | | | | | 0 | 11 | 2574 | 73581 | 0 | 6754 | 0 | 0 | 0 | 1249 | | | | | | | | |
| DaPeng-12 | | | | | | | | 0 | 0 | 16631 | 47635 | 0 | 7699 | 0 | 0 | 0 | 1779 | | | | | | | | |
| DaPeng-10 | | | | | | | | 0 | 34 | 0 | 33809 | 0 | 10777 | 0 | 0 | 0 | 515 | | | | | | | | |
| DaPeng-21 | | | | | | | | 0 | 257 | 704 | 90021 | 0 | 2318 | 0 | 56 | 0 | 300 | | | | | | | | |
| DaPeng-2 | | | | | | | | 0 | 408 | 205 | 146948 | 0 | 1211 | 0 | 46 | 0 | 323 | | | | | | | | |
| DaPeng-2 | | | | | | | | 0 | 213 | 6567 | 106646 | 0 | 3713 | 0 | 0 | 0 | 584 | | | | | | | | |
| DaPeng-4 | | | | | | | | 0 | 53 | 561 | 66193 | 0 | 559 | 0 | 354 | 0 | 801 | | | | | | | | |
| DaPeng-5 | | | | | | | | 0 | 2655 | 0 | 45709 | 0 | 0 | 0 | 249 | 0 | 623 | | | | | | | | |
| DaPeng-6 | | | | | | | | 0 | 1846 | 0 | 54509 | 0 | 58 | 0 | 19 | 0 | 492 | | | | | | | | |
| AS49 - 6 | | | | | | | wt | 0 | 20 | 4742 | 66151 | 0 | 2099 | 0 | 0 | 0 | 345 | | | | | | | | |
| EKVX - 8 | | | | | | | mutant | 0 | 164 | 4424 | 74530 | 0 | 7705 | 0 | 0 | 0 | 2322 | | | | | | | | |
| HCT-116 - 7 | | | | | | | wt | 0 | 173 | 636 | 22256 | 0 | 1578 | 0 | 721 | 0 | 1566 | | | | | | | | |
| HCT-116 - 8 | | | | | | | wt | 0 | 205 | 779 | 29245 | 0 | 2302 | 0 | 0 | 0 | 1781 | | | | | | | | |
| HT29 - 1 | | | | | | | mutant | 0 | 1671 | 1301 | 47637 | 0 | 2761 | 0 | 315 | 0 | 852 | | | | | | | | |
| HT29 - 7 | | | | | | | mutant | 0 | 0 | 0 | 14634 | 0 | 90 | 0 | 95 | 0 | 444 | | | | | | | | |
| HT29 - 8 | | | | | | | mutant | 0 | 45 | 643 | 36186 | 0 | 347 | 0 | 0 | 0 | 459 | | | | | | | | |
| SF339 - 7 | | | | | | | wt | 0 | 254 | 114 | 26009 | 0 | 1532 | 0 | 124 | 0 | 933 | | | | | | | | |
| SF339 - 8 | | | | | | | wt | 0 | 10071 | 1761 | 34166 | 0 | 4118 | 0 | 0 | 0 | 1851 | | | | | | | | |
| SF-268-7 | | | | | | | mutant | 0 | 0 | 2013 | 52411 | 0 | 2540 | 0 | 167 | 0 | 1489 | | | | | | | | |
| SF-268-8 | | | | | | | mutant | 0 | 1385 | 1825 | 39762 | 0 | 4138 | 0 | 126 | 0 | 1371 | | | | | | | | |
| OVCAR-4 - 7 | | | | | | | wt | 0 | 109 | 0 | 24881 | 0 | 534 | 0 | 140 | 0 | 2424 | | | | | | | | |
| OVCAR-4 - 8 | | | | | | | wt | 0 | 0 | 2400 | 56208 | 0 | 6738 | 0 | 0 | 0 | 768 | | | | | | | | |
| OVCAR-5 - 7 | | | | | | | mutant | 0 | 1141 | 660 | 96690 | 0 | 2132 | 0 | 0 | 0 | 3749 | | | | | | | | |
| OVCAR-5 - 8 | | | | | | | wt | 0 | 79 | 1821 | 39762 | 0 | 1 | 0 | 0 | 0 | 2322 | | | | | | | | |
| MCF-7 - 8 | | | | | | | wt | 0 | 204 | 0 | 40597 | 0 | 258 | 0 | 8 | 0 | 342 | | | | | | | | |
| ADR-RES - 8 | | | | | | | mutant | 0 | 108 | 0 | 23503 | 0 | 101 | 0 | 323 | 0 | 1207 | | | | | | | | |
| HuL-6 - 8 | | | | | | | HPV E6 | 0 | 1303 | 1036 | 31952 | 0 | 564 | 0 | 209 | 0 | 1336 | | | | | | | | |
| SW480 - 7 | | | | | | | wt | 0 | 236 | 483 | 28425 | 0 | 1126 | 0 | 89 | 0 | 1435 | | | | | | | | |
| SW480 - 8 | | | | | | | mutant | 0 | 1123 | 0 | 27332 | 0 | 1972 | 0 | 330 | 0 | 879 | | | | | | | | |
| H1299 - 8 | | | | | | | mutant | 0 | 215 | 7268 | 20150 | 0 | 2091 | 0 | 53 | 0 | 724 | | | | | | | | |
| C33A - 7 | | | | | | | mutant | 0 | 1006 | 204 | 10811 | 0 | 9 | 0 | 0 | 0 | 656 | | | | | | | | |
| C33A - 8 | | | | | | | wt | 0 | 1223 | 70434 | 38 | 0 | 3385 | 0 | 215 | 0 | 1853 | | | | | | | | |
| U2OS - 7 | | | | | | | mutant | 0 | 220 | 1497 | 83511 | 0 | 3482 | 0 | 113 | 0 | 970 | | | | | | | | |
| U2OS - 8 | | | | | | | mutant | 0 | 1325 | 826 | 33247 | 0 | 112 | 0 | 38 | 0 | 850 | | | | | | | | |
| HuH6 - 7 | | | | | | | wt | 0 | 86 | 522 | 76356 | 0 | 9382 | 0 | 0 | 0 | 855 | | | | | | | | |
| HuH6 - 8 | | | | | | | wt | 0 | 0 | 530 | 40610 | 0 | 1824 | 0 | 2 | 0 | 1105 | | | | | | | | |
| WI38 - 8 | | | | | | | wt | 0 | 55 | 0 | 82606 | 0 | 142 | 0 | 0 | 0 | 960 | | | | | | | | |
| 456 melanoma RNA | | | | | | | | 56 | 316 | 16715 | 14760 | 157513 | 855 | 80 | 0 | 2438 | | | | | | | | | |
| CR1572 3/17/89 | | | | | | | | 0 | 0 | 154 | 1378 | 926 | 83 | 21 | 0 | 2241 | | | | | | | | | |
| Bep-1 | | | | | | | 84 | 110 | 70 | 107 | 3788 | 616 | 605 | 254 | 0 | 1872 | | | | | | | | | |
| HT369 | | | | | | | | 0 | 33 | 0 | 4338 | 137 | 22 | 506 | 549 | 7852 | | | | | | | | | |
| HT378 | | | | | | | | 0 | 30 | 0 | 4042 | 10 | 0 | 44 | 0 | 3943 | | | | | | | | | |
| HT378 | | | | | | | | 662 | 115 | 251 | 5216 | 14108 | 1123 | 1150 | 133 | 10627 | | | | | | | | | |
| HT308 | | | | | | | | 309 | 183 | 874 | 5319 | 297 | 356 | 0 | 0 | 0 | 0 | | | | | | | | |
| Bov-3 | | | | | | | | 173 | 105 | 0 | 1494 | 249 | 0 | 8 | 0 | 4067 | | | | | | | | | |
| Bov-5 | | | | | | | | 175 | 115 | 220 | 154 | 44 | 0 | 0 | 0 | 2716 | | | | | | | | | |
| Bov-9 | | | | | | | | 177 | 10 | 0 | 1799 | 0 | 54 | 0 | 103 | 3483 | | | | | | | | | |
| n keratinocytes 2/25/92 #10 | | | | | | | | 10 | 0 | 0 | 2152 | 2734 | 0 | 61 | 0 | 506 | | | | | | | | | |
| Bov-10 | | | | | | | | 237 | 87 | 50 | 0 | 4051 | 559 | 416 | 154 | 77 | 2460 | | | | | | | | |
| HTB10 | | | | | | | | 49 | 73 | 621 | 8012 | 740 | 165 | 181 | 6 | 1021 | | | | | | | | | |
| prostate h | | | | | | | | 0 | 0 | 2911 | 3370 | 0 | 518 | 0 | 111 | 1882 | | | | | | | | | |
| hMMV-Q5 pcy A+ | | | | | | | | 0 | 0 | 0 | 45303 | 0 | 0 | 0 | 0 | 0 | 0 | | | | | | | | |
| SA-Q5 (Mundy) pcy A+ | | | | | | | | 235 | 87 | 4366 | 4893 | 295 | 495 | 375 | 11 | 12800 | | | | | | | | | |
| hK pcy A+ | | | | | | | | 532 | 0 | 3011 | 1291 | 6062 | 49 | 769 | 249 | 6785 | | | | | | | | | |
| HCT-116 - 3 | | | | | | | | 630 | 0 | 7825 | 1953 | 8543 | 271 | 1030 | 147 | 4771 | | | | | | | | | |
| HCT-116 - 4 | | | | | | | wt | 0 | 0 | 0 | 23008 | 0 | 1747 | 0 | 0 | 0 | 0 | | | | | | | | |
| HCT-116 - 5 | | | | | | | wt | 0 | 211 | 234 | 30187 | 0 | 5246 | 0 | 52 | 0 | 307 | | | | | | | | |
| HCT-116 - 6 | | | | | | | wt | 0 | 7 | 37 | 34589 | 0 | 2413 | 0 | 0 | 0 | 1024 | | | | | | | | |
| AS49 - 6 | | | | | | | wt | 0 | 186 | 363 | 35088 | 0 | 1998 | 0 | 66 | 0 | 1306 | | | | | | | | |
| HT29 - 3 | | | | | | | wt | 0 | 0 | 0 | 21927 | 0 | 0 | 0 | 0 | 0 | 807 | | | | | | | | |
| EKVX - 6 | | | | | | | mutant | 0 | 302 | 1078 | 19979 | 0 | 153 | 0 | 159 | 0 | 980 | | | | | | | | |
| HT29 - 4 | | | | | | | mutant | 0 | 0 | 41 | 24371 | 0 | 187 | 0 | 92 | 0 | 1103 | | | | | | | | |
| HT29 - 5 | | | | | | | mutant | 0 | 132 | 0 | 25069 | 0 | 464 | 0 | 0 | 0 | 2528 | | | | | | | | |
| HT29 - 6 | | | | | | | mutant | 0 | 31 | 1357 | 74812 | 0 | 629 | 0 | 82 | 0 | 827 | | | | | | | | |
| OVCAR-4 - 3 | | | | | | | wt | 0 | 470 | 0 | 42341 | 0 | 152 | 0 | 0 | 0 | 1335 | | | | | | | | |
| OVCAR-4 - 4 | | | | | | | wt | 0 | 235 | 328 | 29521 | 0 | 5217 | 0 | 0 | 0 | 879 | | | | | | | | |
| OVCAR-4 - 5 | | | | | | | wt | 0 | 438 | 397 | 30765 | 0 | 2562 | 0 | 0 | 0 | 1008 | | | | | | | | |
| OVCAR-4 - 6 | | | | | | | wt | 0 | 100 | 934 | 38317 | 0 | 9800 | 0 | 65 | 0 | 940 | | | | | | | | |
| SF339 - 3 | | | | | | | wt | 0 | 508 | 458 | 18032 | 0 | 312 | 0 | 5151 | 1063 | | | | | | | | | |
| SF339 - 4 | | | | | | | wt | 0 | 112 | 4556 | 32560 | 0 | 1961 | 0 | 0 | 0 | 1253 | | | | | | | | |
| SF339 - 5 | | | | | | | wt | 0 | 0 | 2466 | 27211 | 0 | 2209 | 0 | 36 | 0 | 1062 | | | | | | | | |
| SF339 - 6 | | | | | | | wt | 0 | 38 | 176 | 22964 | 0 | 1587 | 0 | 236 | 0 | 1238 | | | | | | | | |
| OVCAR-5 - 3 | | | | | | | mutant | 0 | 211 | 1013 | 59830 | 0 | 0 | 0 | 262 | 0 | 827 | | | | | | | | |
| OVCAR-5 - 4 | | | | | | | mutant | 0 | 161 | 662 | 27675 | 0 | 1461 | 0 | 0 | 0 | 424 | | | | | | | | |
| OVCAR-5 - 5 | | | | | | | mutant | 0 | 402 | 984 | 18852 | 0 | 1206 | 0 | 362 | 0 | 617 | | | | | | | | |
| OVCAR-5 - 6 | | | | | | | mutant | 0 | 183 | 418 | 8373 | 0 | 453 | 0 | 0 | 0 | 477 | | | | | | | | |
| ADR-RES - 6 | | | | | | | wt | 0 | 34 | 87 | 24265 | 0 | 996 | 0 | 2 | 0 | 579 | | | | | | | | |

Table 3 (cont'd)

| Tissue | Tumor - sym | Normal - sym | Tumor - To | Tumor Cells | Normal | Endose | p53 | SEG 93 | AN | SEG 94 | AN | SEG 97 | HER2 | 100 | AN | SEG 101 | AN | SEG 110 | AN | SEG 111 | AN | SEG 112 | AN | SEG 114 | AN |
|----------------------|-------------|--------------|------------|-------------|--------|--------|-----|--------|------|--------|-------|--------|-------|-------|-------|---------|-------|---------|-------|---------|----|---------|----|---------|----|
| adrenal gland - h | 2 | | | | | | | 0 | 520 | 93171 | 16583 | | 53111 | 3706 | 92946 | | 560 | | 16327 | | | | | | |
| lymph node - h | 3 | | | | | | | 145 | 1220 | 11829 | 24716 | | 19927 | 5389 | 19401 | | 962 | | 19488 | | | | | | |
| bone marrow - h | 3 | | | | | | | 0 | 833 | 3256 | 4004 | | 4161 | 4045 | 16648 | | 1113 | | 4801 | | | | | | |
| mammary gland - h | 5 | | | | | | | 121 | 366 | 949 | 407 | | 452 | 1561 | 1216 | | 553 | | 3951 | | | | | | |
| breast - h | 6 | | | | | | | 480 | 947 | 2451 | 11046 | | 2517 | 5005 | 85845 | | 245 | | 12790 | | | | | | |
| pancreas - h | 6 | | | | | | | 543 | 905 | 1776 | 11768 | | 4259 | 4397 | 19743 | | 1117 | | 11148 | | | | | | |
| coronary artery - h | 7 | | | | | | | 342 | 1137 | 14444 | 44712 | | 4832 | 3900 | 16014 | | 1309 | | 51344 | | | | | | |
| pancreatic gland - h | 8 | | | | | | | 615 | 531 | 4052 | 21435 | | 8617 | 4163 | 27271 | | 1159 | | 19044 | | | | | | |
| testis - h | 9 | | | | | | | 0 | 1302 | 3571 | 20740 | | 4861 | 7201 | 98138 | | 1589 | | 26240 | | | | | | |
| testis - h | 10 | | | | | | | 863 | 818 | 7524 | 4384 | | 8283 | 3481 | 51723 | | 1725 | | 28256 | | | | | | |
| prostate - h | 11 | | | | | | | 1069 | 1190 | 8450 | 16797 | | 9585 | 4326 | 34711 | | 2075 | | 41845 | | | | | | |
| testis - h | 12 | | | | | | | 246 | 1235 | 3569 | 4142 | | 1439 | 4358 | 14560 | | 907 | | 11285 | | | | | | |
| testis - h | 13 | | | | | | | 641 | 468 | 3524 | 7769 | | 2506 | 5648 | 20032 | | 1120 | | 18166 | | | | | | |
| testis - h | 14 | | | | | | | 1164 | 609 | 3315 | 13136 | | 8957 | 5222 | 18162 | | 1638 | | 97915 | | | | | | |
| testis - h | 15 | | | | | | | 349 | 605 | 508 | 3019 | | 533 | 2560 | 11312 | | 1787 | | 13407 | | | | | | |
| muscle - h | 16 | | | | | | | 32 | 708 | 3722 | 3365 | | 1196 | 1481 | 41333 | | 1155 | | 37255 | | | | | | |
| muscle - h | 17 | | | | | | | 0 | 524 | 2431 | 8421 | | 3280 | 2078 | 10571 | | 1713 | | 19616 | | | | | | |
| small intestine - h | 18 | | | | | | | 891 | 386 | 8028 | 14631 | | 4976 | 4012 | 15666 | | 1331 | | 12278 | | | | | | |
| kidney - h | 19 | | | | | | | 1080 | 264 | 1535 | 4310 | | 1760 | 846 | 16499 | | 1055 | | 6030 | | | | | | |
| esophagus - h | 20 | | | | | | | 0 | 428 | 1611 | 8137 | | 1685 | 3116 | 19447 | | 1425 | | 4737 | | | | | | |
| liver - h | 21 | | | | | | | 336 | 348 | 4692 | 6027 | | 3412 | 1391 | 6699 | | 1068 | | 4256 | | | | | | |
| spleen - h | 22 | | | | | | | 0 | 152 | 5215 | 8947 | | 1831 | 1320 | 892 | | 20815 | | | | | | | | |
| lung - h | 23 | | | | | | | 0 | 443 | 2248 | 3728 | | 1851 | 2148 | 6009 | | 1235 | | 8363 | | | | | | |
| stomach - h | 24 | | | | | | | 15430 | 2154 | 35048 | 4231 | | 28181 | 6520 | 67369 | | 890 | | 24003 | | | | | | |
| testis - h | 25 | | | | | | | 790 | 414 | 5036 | 18572 | | 11138 | 4767 | 11603 | | 362 | | 13111 | | | | | | |
| thymus - h | 26 | | | | | | | 703 | 187 | 0 | 239 | | 1152 | 3658 | 4271 | | 801 | | 24405 | | | | | | |
| HPAEC | 27 | | | | | | | 581 | 660 | 1230 | 4184 | | 9196 | 2990 | 21807 | | 910 | | 0 | | | | | | |
| thyroid gland - h | 28 | | | | | | | 161 | 516 | 0 | 390 | | 1052 | 3123 | 1920 | | 723 | | 0 | | | | | | |
| RPTC | 29 | | | | | | | 586 | 740 | 4364 | 9891 | | 10717 | 2098 | 13272 | | 1555 | | 56690 | | | | | | |
| trachea - h | 30 | | | | | | | 0 | 544 | 250 | 35 | | 115 | 3044 | 1023 | | 1182 | | 0 | | | | | | |
| HMEC | 31 | | | | | | | 0 | 2915 | 6459 | 3860 | | 1347 | 20990 | 1100 | | 67028 | | 0 | | | | | | |
| uterus - h | 32 | | | | | | | 0 | 299 | 0 | 454 | | 3409 | 1110 | 805 | | 0 | | 0 | | | | | | |
| HPAEC | 33 | | | | | | | 0 | 451 | 0 | 312 | | 222 | 1822 | 885 | | 620 | | 0 | | | | | | |
| pancreas - h | 34 | | | | | | | 746 | 473 | 443 | 301 | | 11 | 1061 | 683 | | 915 | | 1325 | | | | | | |
| peritoneum - h | 35 | | | | | | | 0 | 375 | 160 | 0 | | 1441 | 1996 | 720 | | 0 | | 0 | | | | | | |
| stomach muscle - h | 36 | | | | | | | 0 | 842 | 0 | 363 | | 0 | 3211 | 1392 | | 1054 | | 901 | | | | | | |
| testis - h | 37 | | | | | | | 0 | 338 | 1343 | 0 | | 1194 | 3263 | 658 | | 145 | | 0 | | | | | | |
| heart - h | 38 | | | | | | | 143 | 527 | 0 | 499 | | 362 | 2819 | 541 | | 1215 | | 0 | | | | | | |
| thymus - h | 39 | | | | | | | 996 | 293 | 5181 | 136 | | 2534 | 0 | 1094 | | 0 | | 0 | | | | | | |
| duodenum - h | 40 | | | | | | | 629 | 409 | 0 | 5731 | | 1760 | 1771 | 2223 | | 0 | | 0 | | | | | | |
| testis - h | 41 | | | | | | | 0 | 421 | 1541 | 0 | | 145 | 1660 | 1341 | | 1205 | | 0 | | | | | | |
| salivary gland - h | 42 | | | | | | | 1653 | 626 | 2190 | 425 | | 3678 | 2317 | 978 | | 1846 | | 0 | | | | | | |
| testis - h | 43 | | | | | | | 0 | 323 | 0 | 0 | | 734 | 53 | 348 | | 0 | | 0 | | | | | | |
| MT213-normal | 44 | | | | | | | 0 | 0 | 283 | 151 | | 0 | 120 | 0 | | 134 | | 0 | | | | | | |
| MT213-normal | | | | | | | | 0 | 0 | 0 | 18 | | 0 | 83 | 2404 | | 165 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 4165 | 5699 | 345 | 634 | | 302 | 8771 | 296 | | 34191 | | 16340 | | | | | | |
| MT151-normal | | | | | | | | 7285 | 3210 | 12525 | 308 | | 60 | 4805 | 182 | | 1521 | | 16396 | | | | | | |
| MT151-normal | | | | | | | | 0 | 254 | 82 | 225 | | 35 | 297 | 64 | | 558 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 0 | 32 | 268 | | 0 | 248 | 0 | | 452 | | 264 | | | | | | |
| MT151-normal | | | | | | | | 0 | 346 | 0 | 0 | | 0 | 746 | 0 | | 1664 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 11 | 19 | 24 | | 91 | 45 | 836 | | 0 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 91 | 0 | 87 | | 0 | 711 | 0 | | 687 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 1607 | 2645 | 0 | 1912 | | 109 | 2629 | 456 | | 1452 | | 7258 | | | | | | |
| MT151-normal | | | | | | | | 0 | 591 | 0 | 1711 | | 0 | 118 | 411 | | 428 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 309 | 4778 | 56 | 727 | | 0 | 1869 | 92 | | 1924 | | 9521 | | | | | | |
| MT151-normal | | | | | | | | 218 | 45 | 0 | 0 | | 0 | 72 | 755 | | 0 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 780 | 0 | 283 | | 239 | 2579 | 21 | | 1311 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 2610 | 1322 | 774 | 2029 | | 2189 | 4262 | 471 | | 1087 | | 2660 | | | | | | |
| MT151-normal | | | | | | | | 832 | 14 | 0 | 1132 | | 1803 | 2543 | 0 | | 701 | | 1532 | | | | | | |
| MT151-normal | | | | | | | | 195 | 271 | 0 | 249 | | 2547 | 2242 | 333 | | 730 | | 2522 | | | | | | |
| MT151-normal | | | | | | | | 0 | 0 | 0 | 153 | | 47 | 58 | 251 | | 1072 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 59 | 551 | 47 | 125 | | 242 | 100 | 167 | | 452 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 306 | 810 | 154 | 464 | | 86 | 1074 | 0 | | 401 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 79 | 0 | 397 | | 200 | 520 | 535 | | 249 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 1875 | 0 | 1864 | | 675 | 1375 | 49 | | 8331 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 0 | 306 | 123 | | 72 | 306 | 254 | | 998 | | 228 | | | | | | |
| MT151-normal | | | | | | | | 7749 | 8516 | 2195 | 2065 | | 3729 | 4087 | 1220 | | 1487 | | 4479 | | | | | | |
| MT151-normal | | | | | | | | 298 | 4982 | 0 | 2022 | | 2522 | 2776 | 0 | | 2119 | | 1673 | | | | | | |
| MT151-normal | | | | | | | | 0 | 260 | 0 | 807 | | 515 | 399 | 861 | | 631 | | 480 | | | | | | |
| MT151-normal | | | | | | | | 1237 | 1442 | 0 | 1965 | | 100 | 2031 | 75 | | 1715 | | 85 | | | | | | |
| MT151-normal | | | | | | | | 0 | 0 | 0 | 1415 | | 265 | 810 | 0 | | 548 | | 85 | | | | | | |
| MT151-normal | | | | | | | | 1424 | 482 | 0 | 3317 | | 685 | 1687 | 277 | | 901 | | 2243 | | | | | | |
| MT151-normal | | | | | | | | 2289 | 171 | 0 | 0 | | 855 | 289 | 455 | | 801 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 744 | 0 | 0 | | 249 | 1352 | 374 | | 864 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 0 | 14 | 667 | 0 | | 0 | 407 | 181 | | 801 | | 0 | | | | | | |
| MT151-normal | | | | | | | | 275 | 275 | 0 | 0 | | 500 | 113 | 266 | | 154 | | 563 | | | | | | |
| MT151-normal | | | | | | | | 0 | 0 | 1147 | 161 | | 0 | 0 | 245 | | 738 | | 752 | | | | | | |
| MT151-normal | | | | | | | | 239 | 239 | 0 | 300 | | 222 | 599 | 531 | | 2817 | | 1460 | | | | | | |
| MT151-normal | | | | | | | | 0 | 89 | 86 | 127 | | 40 | 0 | 481 | | 751 | | | | | | | | |

184
Table 3 (cont'd)

| Tissue | Tumor + ym | Normal + ym | Tumor - to | Tumor Cells | Normal | Endox | p53 | SEQ 95 | AA | SEQ 96 | AA | SEQ 97 | HB | SEQ 100 | AA | SEQ 101 | AA | SEQ 110 | AA | SEQ 111 | AA | SEQ 112 | AA | SEQ 114 | AA |
|------------------------------|------------|-------------|------------|-------------|--------|-------|-----|--------|------|--------|------|--------|-------|---------|------|---------|----|---------|----|---------|----|---------|----|---------|----|
| CAL3 | | | | 166 | | | | | | | | | | | | | | | | | | | | | |
| T66-0 | | | | 166 | | | | 229 | 0 | 377 | 0 | 308 | 0 | 131 | 0 | 1115 | 0 | 713 | 0 | 82 | 0 | 303 | 0 | | |
| L470 | | | | 169 | | | | 0 | 152 | 14 | 104 | 5501 | 1079 | 0 | 768 | 0 | | | | | | | | | |
| Kan-3 | | | | 171 | | | | 0 | 3 | 150 | 65 | 0 | 338 | 0 | 530 | 0 | | | | | | | | | |
| CRL1441 RNA 6/30 | | | | 181 | | | | 31 | 447 | 0 | 1 | 81 | 747 | 0 | 526 | 0 | | | | | | | | | |
| T811 untreated + DMSO | | | | 183 | | | | 0 | 201 | 0 | 0 | 173 | 109 | 0 | 423 | 0 | | | | | | | | | |
| KB poly A+ | | | | 191 | | | | 0 | 0 | 263 | 279 | 1030 | 237 | 0 | 448 | 0 | | | | | | | | | |
| HOS poly A+ | | | | 196 | | | | 0 | 0 | 131 | 139 | 162 | 260 | 0 | 474 | 0 | | | | | | | | | |
| ACHN | | | | 198 | | | | 118 | 293 | 0 | 87 | 1048 | 685 | 0 | 553 | 0 | | | | | | | | | |
| UACC-62 | | | | 200 | | | | 221 | 691 | 0 | 64 | 1808 | 1271 | 161 | 608 | 0 | | | | | | | | | |
| MCF-7ADRI-RES | | | | 202 | | | | 0 | 76 | 137 | 0 | 167 | 136 | 172 | 257 | 0 | | | | | | | | | |
| UTOS (Mundy) poly A+ | | | | 204 | | | | 305 | 524 | 946 | 0 | 73 | 3428 | 156 | 431 | 0 | | | | | | | | | |
| WISH (Coker) poly A+ | | | | 206 | | | | 0 | 0 | 808 | 0 | 293 | 474 | 0 | 197 | 10 | | | | | | | | | |
| 458 modulo mRNA | | | | 208 | | | | 712 | 1711 | 0 | 351 | 369 | 1345 | 0 | 758 | 0 | | | | | | | | | |
| CCL137 RNA 3/21/80 | | | | 218 | | | | 247 | 151 | 680 | 0 | 27 | 168 | 0 | 452 | 0 | | | | | | | | | |
| WI-36 72h 0.5%FBS 24h 10%FBS | | | | 219 | | | | 0 | 186 | 0 | 114 | 30 | 115 | 0 | 305 | 0 | | | | | | | | | |
| CRL1441 + TPA (24h) 6/30 | | | | 220 | | | | 0 | 0 | 92 | 136 | 41 | 322 | 0 | 477 | 0 | | | | | | | | | |
| Kan-1 | | | | 221 | | | | 0 | 80 | 0 | 5 | 42 | 212 | 164 | 577 | 0 | | | | | | | | | |
| Kan-2 | | | | 223 | | | | 0 | 140 | 161 | 117 | 1601 | 117 | 0 | 478 | 0 | | | | | | | | | |
| Kan-4 | | | | 225 | | | | 0 | 172 | 205 | 31 | 0 | 86 | 0 | 457 | 0 | | | | | | | | | |
| HOP-82 | | | | 241 | | | | 0 | 0 | 197 | 155 | 365 | 80 | 0 | 66 | 1898 | | | | | | | | | |
| MDA-T-4 | | | | 242 | | | | 0 | 0 | 173 | 504 | 2918 | 787 | 524 | 294 | 0 | | | | | | | | | |
| ECVx | | | | 243 | | | | 862 | 302 | 19 | 274 | 720 | 376 | 0 | 870 | 0 | | | | | | | | | |
| Hs 460 | | | | 244 | | | | 2486 | 529 | 0 | 272 | 5737 | 330 | 65 | 18 | 917 | 0 | | | | | | | | |
| NCI-H460 | | | | 245 | | | | 27 | 233 | 624 | 424 | 2576 | 193 | 0 | 337 | 0 | | | | | | | | | |
| HPM1-4236 | | | | 246 | | | | 0 | 590 | 847 | 148 | 1672 | 0 | 0 | 460 | 0 | | | | | | | | | |
| AS54WATCC | | | | 247 | | | | 225 | 106 | 0 | 312 | 249 | 0 | 548 | 981 | 0 | | | | | | | | | |
| SR | | | | 248 | | | | 0 | 122 | 0 | 229 | 298 | 923 | 0 | 425 | 0 | | | | | | | | | |
| OVCAR-3 | | | | 249 | | | | 0 | 0 | 1127 | 321 | 3870 | 467 | 215 | 306 | 270 | 0 | | | | | | | | |
| HCT-15 | | | | 250 | | | | 18 | 423 | 54 | 448 | 1543 | 531 | 362 | 484 | 6992 | 0 | | | | | | | | |
| OVCAR-4 | | | | 251 | | | | 0 | 84 | 423 | 79 | 463 | 453 | 0 | 41 | 0 | | | | | | | | | |
| UO-31 | | | | 252 | | | | 197 | 270 | 0 | 207 | 62 | 34 | 0 | 41 | 0 | | | | | | | | | |
| OVCAR-5 | | | | 253 | | | | 0 | 816 | 0 | 73 | 8728 | 1339 | 0 | 351 | 305 | 0 | | | | | | | | |
| SN12C | | | | 254 | | | | 690 | 366 | 992 | 0 | 1416 | 396 | 452 | 567 | 0 | | | | | | | | | |
| OVCAR-8 | | | | 255 | | | | 753 | 0 | 0 | 19 | 153 | 245 | 0 | 276 | 0 | | | | | | | | | |
| LOX IMVI | | | | 256 | | | | 227 | 541 | 454 | 732 | 3168 | 614 | 357 | 703 | 0 | | | | | | | | | |
| HQROV1 | | | | 257 | | | | 0 | 660 | 554 | 454 | 1607 | 399 | 189 | 626 | 0 | | | | | | | | | |
| SK-MEL-2 | | | | 258 | | | | 0 | 212 | 0 | 63 | 47 | 346 | 0 | 204 | 0 | | | | | | | | | |
| SK-CV-3 | | | | 259 | | | | 0 | 572 | 0 | 0 | 634 | 448 | 415 | 653 | 0 | | | | | | | | | |
| SK-MEL-5 | | | | 260 | | | | 211 | 0 | 0 | 0 | 1528 | 325 | 0 | 453 | 0 | | | | | | | | | |
| SF-539 | | | | 261 | | | | 0 | 352 | 0 | 156 | 2049 | 1651 | 0 | 1121 | 0 | | | | | | | | | |
| SK-MEL-28 | | | | 262 | | | | 0 | 894 | 1839 | 0 | 1332 | 1027 | 0 | 937 | 0 | | | | | | | | | |
| K-562 | | | | 263 | | | | 97 | 0 | 789 | 267 | 473 | 81 | 32 | 544 | 383 | 0 | | | | | | | | |
| UACC-257 | | | | 264 | | | | 0 | 0 | 70 | 2198 | 505 | 0 | 493 | 0 | 0 | 0 | | | | | | | | |
| M14 | | | | 265 | | | | 496 | 0 | 0 | 70 | 414 | 119 | 114 | 186 | 0 | | | | | | | | | |
| MCF7 | | | | 267 | | | | 472 | 0 | 0 | 2572 | 17839 | 1425 | 0 | 1304 | 0 | | | | | | | | | |
| MDA-MB-435 | | | | 268 | | | | 0 | 73 | 0 | 138 | 1633 | 109 | 0 | 96 | 0 | | | | | | | | | |
| MT279 | | | | 270 | | | | 0 | 628 | 0 | 41 | 0 | 1085 | 0 | 800 | 490 | 0 | | | | | | | | |
| MDA-N | | | | 271 | | | | 76 | 276 | 0 | 0 | 1375 | 488 | 647 | 221 | 0 | | | | | | | | | |
| V79 poly A+ | | | | 273 | | | | 0 | 810 | 527 | 318 | 1534 | 1167 | 0 | 1461 | 1871 | 0 | | | | | | | | |
| KHOS poly A+ | | | | 289 | | | | 0 | 158 | 187 | 171 | 233 | 1831 | 0 | 513 | 0 | | | | | | | | | |
| HTB36 24h TPA RNA 6/27 | | | | 300 | | | | 0 | 303 | 85 | 218 | 37 | 0 | 404 | 0 | 0 | 0 | | | | | | | | |
| HELA-EXP-031899 | | | | 313 | | | | 0 | 0 | 207 | 141 | 0 | 0 | 0 | 209 | 0 | | | | | | | | | |
| HTB36 6h RNA | | | | 322 | | | | 605 | 1211 | 0 | 129 | 225 | 1206 | 0 | 1575 | 3066 | 0 | | | | | | | | |
| HTB37 | | | | 323 | | | | 0 | 245 | 0 | 227 | 211 | 117 | 0 | 276 | 0 | | | | | | | | | |
| 458 modulo RNA | | | | 324 | | | | 359 | 1654 | 0 | 0 | 56 | 1282 | 0 | 901 | 4155 | 0 | | | | | | | | |
| NCI-M226 | | | | 336 | | | | 0 | 77 | 0 | 0 | 3462 | 464 | 0 | 514 | 0 | | | | | | | | | |
| HOP-82 | | | | 337 | | | | 0 | 0 | 219 | 657 | 412 | 360 | 0 | 16 | 0 | | | | | | | | | |
| MDA-MB-231 | | | | 338 | | | | 663 | 0 | 0 | 936 | 12037 | 4891 | 0 | 1033 | 3276 | 0 | | | | | | | | |
| U251 | | | | 339 | | | | 2821 | 1673 | 53 | 3315 | 26597 | 11907 | 1155 | 1018 | 2164 | 0 | | | | | | | | |
| PT cells poly A+ | | | | 340 | | | | 136 | 0 | 0 | 292 | 659 | 229 | 26 | 144 | 0 | | | | | | | | | |
| PC-3 | | | | 341 | | | | 363 | 1320 | 0 | 642 | 3005 | 1672 | 0 | 1051 | 958 | 0 | | | | | | | | |
| HCC-2998 | | | | 343 | | | | 300 | 845 | 283 | 44 | 1152 | 493 | 0 | 465 | 0 | | | | | | | | | |
| SW-620 | | | | 345 | | | | 307 | 1338 | 0 | 20 | 1534 | 792 | 0 | 423 | 0 | | | | | | | | | |
| HT192 | | | | 346 | | | | 0 | 232 | 109 | 0 | 217 | 0 | 7 | 86 | 0 | | | | | | | | | |
| COLO 205 | | | | 347 | | | | 0 | 945 | 0 | 169 | 827 | 87 | 115 | 396 | 0 | | | | | | | | | |
| HT118 | | | | 348 | | | | 0 | 309 | 41 | 0 | 212 | 0 | 446 | 0 | 0 | 0 | | | | | | | | |
| KM-12 | | | | 349 | | | | 0 | 1263 | 0 | 56 | 980 | 372 | 150 | 181 | 0 | | | | | | | | | |
| HT151 | | | | 350 | | | | 0 | 476 | 0 | 0 | 427 | 0 | 932 | 725 | 0 | | | | | | | | | |
| A498 | | | | 351 | | | | 453 | 2054 | 628 | 277 | 273 | 587 | 299 | 572 | 1028 | 0 | | | | | | | | |
| HT293 | | | | 352 | | | | 0 | 491 | 163 | 4351 | 54 | 709 | 4 | 1068 | 0 | | | | | | | | | |
| RJF 393 | | | | 353 | | | | 173 | 1830 | 0 | 96 | 446 | 195 | 279 | 638 | 1493 | 0 | | | | | | | | |
| TK-10 | | | | 355 | | | | 4314 | 2783 | 0 | 658 | 3339 | 4922 | 402 | 1376 | 8137 | 0 | | | | | | | | |
| Mammary-3M | | | | 357 | | | | 1135 | 4390 | 0 | 1484 | 22112 | 4961 | 1635 | 1624 | 2340 | 0 | | | | | | | | |
| Mo 578T | | | | 359 | | | | 0 | 458 | 0 | 578 | 205 | 142 | 545 | 354 | 0 | | | | | | | | | |
| HT213 | | | | 50 | | | | 0 | 951 | 949 | 257 | 17 | 1399 | 0 | 249 | 0 | | | | | | | | | |
| HT288 | | | | 52 | | | | 0 | 502 | 0 | 0 | 2784 | 1622 | 190 | 435 | 0 | | | | | | | | | |
| HT139 | | | | 54 | | | | 0 | 648 | 130 | 37 | 0 | 355 | 0 | 354 | 0 | | | | | | | | | |
| HT155 | | | | 56 | | | | 0 | 260 | 0 | 397 | 752 | 0 | 925 | 0 | 0 | 0 | | | | | | | | |
| HT163 | | | | 58 | | | | 0 | 299 | 0 | 47 | 0 | 870 | 0 | 482 | 0 | | | | | | | | | |
| HT170 | | | | 60 | | | | 402 | 2258 | 0 | 412 | 26 | 1722 | 72 | 1136 | 0 | | | | | | | | | |
| HT172 | | | | 62 | | | | 0 | 1113 | 0 | 0 | 411 | 827 | 0 | 698 | 0 | | | | | | | | | |
| HT138 | | | | 63 | | | | 0 | 512 | 76 | 254 | | | | | | | | | | | | | | |

185
Table 3 (contd)

| Tissue | Tumor sym | Normal sym | Tumor - to | Tumor cells | Normal | Endos | p53 | SEQ 85 AA | SEQ 96 AA | SEQ 97 Hb | SEQ 102 AREG | SEQ 101 AREG | SEQ 110 AREG | SEQ 111 AREG | SEQ 112 AREG | SEQ 114 AA |
|--------------------------|-----------|------------|------------|-------------|--------|-------|--------|-----------|-----------|-----------|--------------|--------------|--------------|--------------|--------------|------------|
| Hu 578T | | | | | | | | 2829 | 943 | 0 | 1708 | 2068 | 12004 | 10483 | 6651 | 14782 |
| MCF-7/ADR-RES | 153 | | | | | | | 491 | 517 | 1977 | 891 | 696 | 10679 | 6354 | 692 | 0 |
| MCF-7 | 151 | | | | | | | 5433 | 1235 | 160 | 6856 | 3069 | 25634 | 2094 | 1399 | 2238 |
| M14 | 149 | | | | | | | 3831 | 0 | 459 | 2401 | 1993 | 2416 | 1359 | 1031 | 0 |
| UACC-29 | 147 | | | | | | | 1023 | 305 | 1259 | 2776 | 2137 | 11053 | 6220 | 679 | 947 |
| UACC-42 | 145 | | | | | | | 2545 | 157 | 726 | 756 | 1215 | 4403 | 2499 | 585 | 429 |
| SK-MEL-28 | 144 | | | | | | | 5634 | 60 | 3906 | 1173 | 721 | 3058 | 1531 | 805 | 2945 |
| UO-31 | 143 | | | | | | | 5324 | 487 | 3107 | 504 | 442 | 3090 | 1020 | 1534 | 1197 |
| SK-MEL-5 | 142 | | | | | | | 1336 | 0 | 1009 | 2261 | 2826 | 16384 | 2894 | 801 | 1366 |
| KM-12 | 141 | | | | | | | 261 | 319 | 0 | 489 | 0 | 3403 | 379 | 443 | 0 |
| SK-MEL-2 | 140 | | | | | | | 2614 | 185 | 1844 | 1741 | 479 | 19972 | 1717 | 918 | 3611 |
| MCT-15 | 139 | | | | | | | 4882 | 486 | 855 | 1930 | 369 | 8936 | 6821 | 979 | 1630 |
| Melmo-3M | 138 | | | | | | | 1296 | 46 | 565 | 731 | 1145 | 7970 | 2354 | 9431 | 2899 |
| COLO-205 | 137 | | | | | | | 3539 | 181 | 1993 | 1664 | 1417 | 11150 | 231 | 1214 | 1103 |
| LOX-BM1 | 136 | | | | | | | 3524 | 52 | 1973 | 1526 | 677 | 23802 | 2457 | 967 | 1995 |
| SW-620 | 135 | | | | | | | 4591 | 493 | 1295 | 1150 | 826 | 12216 | 5716 | 850 | 1756 |
| TK-10 | 134 | | | | | | | 4646 | 318 | 1845 | 685 | 494 | 9644 | 2032 | 821 | 1147 |
| MCT-116 | 133 | | | | | | | 1224 | 304 | 579 | 1524 | 323 | 6640 | 3551 | 768 | 0 |
| Hb6-0 | 132 | | | | | | | 2284 | 162 | 1883 | 628 | 792 | 11840 | 2318 | 722 | 0 |
| MCC-2908 | 131 | | | | | | | 2684 | 29 | 0 | 1232 | 719 | 5639 | 859 | 909 | 0 |
| ACHN | 130 | | | | | | | 2287 | 488 | 2048 | 1070 | 936 | 36209 | 2954 | 652 | 0 |
| PC-3 | 129 | | | | | | | 5813 | 370 | 0 | 719 | 646 | 13946 | 25991 | 543 | 0 |
| U373-303 | 128 | | | | | | | 614 | 317 | 8314 | 911 | 540 | 2671 | 7592 | 524 | 105 |
| DU-145 | 127 | | | | | | | 1412 | 83 | 621 | 506 | 461 | 3331 | 1531 | 666 | 312 |
| Caki-1 | 126 | | | | | | | 2183 | 811 | 0 | 1338 | 635 | 8406 | 3126 | 507 | 1596 |
| SR | 125 | | | | | | | 34711 | 320 | 0 | 841 | 330 | 19003 | 1163 | 345 | 841 |
| A439 | 124 | | | | | | | 5481 | 0 | 1125 | 1967 | 269 | 26934 | 10429 | 628 | 1032 |
| APM1-8226 | 123 | | | | | | | 1951 | 46 | 44 | 226 | 354 | 1926 | 0 | 563 | 854 |
| SN12C | 122 | | | | | | | 2060 | 194 | 802 | 178 | 1833 | 11140 | 1038 | 634 | 937 |
| HL-60 | 121 | | | | | | | 930 | 0 | 0 | 294 | 545 | 2164 | 395 | 634 | 0 |
| MOLT-4 | 120 | | | | | | | 5683 | 0 | 1010 | 522 | 1507 | 4271 | 753 | 1295 | 0 |
| OVCA8-5 | 119 | | | | | | | 1590 | 119 | 1759 | 1666 | 2515 | 8853 | 1900 | 525 | 5625 |
| K-562 | 118 | | | | | | | 3767 | 0 | 0 | 850 | 252 | 6345 | 1028 | 1001 | 266 |
| OVCA8-4 | 117 | | | | | | | 1254 | 284 | 0 | 1029 | 2229 | 11490 | 3963 | 1253 | 657 |
| CCRP-CEM | 116 | | | | | | | 6623 | 86 | 1599 | 2572 | 1628 | 25692 | 2316 | 961 | 1348 |
| OVCA8-3 | 115 | | | | | | | 2090 | 150 | 1653 | 934 | 1562 | 12158 | 1242 | 552 | 0 |
| SF-539 | 114 | | | | | | | 3527 | 457 | 10 | 367 | 16956 | 833 | 863 | 1458 | 0 |
| HOP-62 | 113 | | | | | | | 4551 | 0 | 1559 | 673 | 265 | 19248 | 3406 | 287 | 1027 |
| SF-295 | 112 | | | | | | | 2817 | 539 | 75 | 1118 | 801 | 17954 | 1580 | 941 | 0 |
| AS49/ATCC | 111 | | | | | | | 1680 | 940 | 1723 | 2304 | 1701 | 30228 | 3221 | 1074 | 751 |
| SF-768 | 110 | | | | | | | 2259 | 208 | 1443 | 583 | 1814 | 11939 | 4509 | 627 | 1666 |
| NCH-H527 | 109 | | | | | | | 1264 | 8 | 1176 | 1767 | 1721 | 7210 | 1466 | 978 | 1034 |
| U251 | 108 | | | | | | | 2200 | 209 | 729 | 977 | 739 | 8651 | 3516 | 526 | 2250 |
| MCH-H460 | 107 | | | | | | | 2274 | 449 | 1277 | 926 | 936 | 17629 | 1892 | 676 | 0 |
| SNB-75 | 106 | | | | | | | 1146 | 228 | 0 | 405 | 289 | 4322 | 1334 | 723 | 0 |
| SNB-19 | 105 | | | | | | | 3368 | 435 | 0 | 3625 | 1047 | 20442 | 338 | 555 | 327 |
| NCH-H226 | 104 | | | | | | | 2006 | 316 | 0 | 1663 | 455 | 4358 | 2106 | 812 | 1908 |
| SK-OV-3 | 103 | | | | | | | 6463 | 125 | 0 | 1140 | 759 | 4785 | 1552 | 1091 | 0 |
| MCH-H23 | 102 | | | | | | | 6105 | 418 | 0 | 1085 | 615 | 13274 | 5271 | 547 | 3219 |
| K562OV1 | 101 | | | | | | | 6603 | 311 | 0 | 1182 | 841 | 7912 | 446 | 380 | 8 |
| ERXV | 99 | | | | | | | 212 | 0 | 0 | 1683 | 959 | 10757 | 0 | 493 | 0 |
| OVCA8-2 | 98 | | | | | | | 1881 | 170 | 77 | 1733 | 915 | 17090 | 1757 | 340 | 842 |
| HOP-92 | 97 | | | | | | | 3654 | 0 | 477 | 422 | 150 | 7006 | 376 | 162 | 0 |
| h. Bcr/AbMyb 3/1/92 #12 | 48 | | | | | | | 2307 | 154 | 0 | 686 | 878 | 13230 | 5619 | 681 | 481 |
| h. anti-SMAC 10/1/92 #17 | 47 | | | | | | | 269 | 19 | 109 | 231 | 0 | 1286 | 802 | 1342 | 0 |
| h. anti-Myb 2/2/92 #10 | 46 | | | | | | | 534 | 336 | 0 | 183 | 62 | 5234 | 1824 | 1436 | 7982 |
| TCOP | 26 | | | | | | | 1066 | 727 | 4716 | 636 | 2721 | 1945 | 34 | 1742 | 0 |
| AS49-1 | | | | | | | wt | 0 | 0 | 0 | 5421 | 18 | 0 | 353 | 825 | 0 |
| AS49-3 | | | | | | | wt | 0 | 0 | 0 | 4212 | 30 | 0 | 0 | 402 | 0 |
| AS49-4 | | | | | | | wt | 0 | 0 | 0 | 5323 | 49 | 0 | 587 | 404 | 0 |
| AS49-5 | | | | | | | wt | 0 | 0 | 0 | 2172 | 210 | 0 | 50 | 635 | 0 |
| AS49-7 | | | | | | | wt | 0 | 0 | 0 | 162 | 118 | 0 | 830 | 563 | 0 |
| ERXV-1 | | | | | | | mutant | 0 | 0 | 0 | 1343 | 0 | 0 | 428 | 617 | 0 |
| ERXV-4 | | | | | | | mutant | 0 | 0 | 0 | 43690 | 11 | 0 | 557 | 705 | 0 |
| ERXV-5 | | | | | | | mutant | 0 | 0 | 0 | 934 | 0 | 0 | 0 | 706 | 0 |
| ERXV-7 | | | | | | | mutant | 0 | 0 | 0 | 0 | 207 | 0 | 283 | 758 | 0 |
| MCF-7-1 | | | | | | | wt | 0 | 0 | 0 | 1578 | 72 | 0 | 126 | 802 | 0 |
| MCF-7-3 | | | | | | | wt | 0 | 0 | 0 | 718 | 64 | 0 | 0 | 621 | 0 |
| MCF-7-4 | | | | | | | wt | 0 | 0 | 0 | 5245 | 85 | 0 | 536 | 641 | 0 |
| MCF-7-5 | | | | | | | wt | 0 | 0 | 0 | 1155 | 73 | 0 | 353 | 895 | 0 |
| MCF-7-7 | | | | | | | wt | 0 | 0 | 0 | 1050 | 189 | 0 | 0 | 685 | 0 |
| ADR-RES-1 | | | | | | | wt | 0 | 0 | 0 | 1327 | 145 | 0 | 217 | 659 | 0 |
| ADR-RES-3 | | | | | | | mutant | 0 | 0 | 0 | 3845 | 0 | 0 | 16 | 2343 | 0 |
| ADR-RES-4 | | | | | | | mutant | 0 | 0 | 0 | 525 | 99 | 0 | 169 | 966 | 0 |
| ADR-RES-5 | | | | | | | mutant | 0 | 0 | 0 | 951 | 0 | 0 | 0 | 875 | 0 |
| ADR-RES-7 | | | | | | | mutant | 0 | 0 | 0 | 472 | 112 | 0 | 0 | 0 | 0 |
| WI38-1 | | | | | | | wt | 0 | 0 | 0 | 7502 | 0 | 0 | 329 | 670 | 0 |
| WI38-3 | | | | | | | wt | 0 | 0 | 0 | 222 | 0 | 0 | 2197 | 854 | 0 |
| WI38-4 | | | | | | | wt | 0 | 0 | 0 | 217 | 672 | 0 | 561 | 555 | 0 |
| WI38-5 | | | | | | | wt | 0 | 0 | 0 | 751 | 79 | 0 | 548 | 545 | 0 |
| WI38-7 | | | | | | | wt | 0 | 0 | 0 | 3721 | 114 | 0 | 1814 | 829 | 0 |
| HLA-1 | | | | | | | wt | 0 | 0 | 0 | 4617 | 0 | 0 | 0 | 956 | 0 |
| HLA-3 | | | | | | | wt | 0 | 0 | 0 | 12621 | 108 | 0 | 0 | 1073 | 0 |
| HLA-4 | | | | | | | wt | 0 | 0 | 0 | 643 | 263 | 0 | 74 | 88 | 0 |
| HLA-5 | | | | | | | wt | 0 | 0 | 0 | 3211 | 270 | 0 | 5015 | 8711 | 0 |
| HLA-7 | | | | | | | wt | 0 | 0 | 0 | 1166 | 818 | 0 | 1402 | 1155 | 0 |
| H1299-1 | | | | | | | wt | 0 | 0 | 0 | 1049 | 450 | 0 | 0 | 801 | 0 |
| H1299-3 | | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 702 | 0 |
| H1299-4 | | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 0 | 212 | 998 | 0 |
| H1299-5 | | | | | | | mutant | 0 | 0 | 0 | 2070 | 520 | 0 | 147 | 1242 | 0 |
| H1299-7 | | | | | | | mutant | 0 | 0 | 0 | 1606 | 183 | 0 | 958 | 578 | 0 |
| AS49-2 | | | | | | | wt | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 719 | 0 |
| ERXV-2 | | | | | | | wt | 0 | 0 | 0 | 470 | 0 | 0 | 409 | 565 | 0 |
| HCT-116-1 | | | | | | | wt | 0 | 0 | 0 | 2003 | 86 | 0 | 0 | 373 | 0 |
| HCT-116-2 | | | | | | | wt | 0 | 0 | 0 | 5597 | 143 | 0 | 13271 | 1078 | 0 |
| HT29-2 | | | | | | | wt | 0 | 0 | 0 | 3756 | 44 | 0 | 20631 | 5161 | 0 |
| SF539-1 | | | | | | | wt | 0 | 0 | 0 | 1380 | 188 | 0 | 1005 | 1045 | 0 |
| SF539-2 | | | | | | | wt | 0 | 0 | 0 | 1849 | 198 | 0 | 2201 | 659 | 0 |
| SF-268-1 | | | | | | | wt | 0 | 0 | 0 | 2474 | 10 | 0 | 397 | 7191 | 0 |
| SF-268-2 | | | | | | | wt | 0 | 0 | 0 | 317 | 2004 | 0 | 1212 | 595 | 0 |
| OVCA8-1 | | | | | | | wt | 0 | 0 | 0 | 550 | 285 | 0 | 4511 | 9531 | 0 |
| OVCA8-2 | | | | | | | wt | 0 | 0 | 0 | 802 | 619 | 0 | 375 | 1271 | 0 |
| OVCA8-3 | | | | | | | wt | 0 | 0 | 0 | 1543 | 196 | 0 | 214 | 1200 | 0 |
| OVCA8-4 | | | | | | | wt | 0 | 0 | 0 | 581 | 154 | 0 | 430 | 914 | 0 |
| OVCA8-5 | | | | | | | wt | 0 | 0 | 0 | 10 | 90 | 0 | | | |

| Tissue | Tumor - ym | Normal - ym | Tumor - to | Tumor cells | Normal | Endos | p31 | SEQ 95 | AA | SEQ 96 | AA | SEQ 97 | HSE | SEQ 100 | AA | SEQ 110 | AA | SEQ 111 | AA | SEQ 112 | AA | SEQ 114 | AA |
|-------------|------------|-------------|------------|-------------|--------|-------|--------|--------|----|--------|----|--------|-----|---------|----|---------|------|---------|----|---------|----|---------|----|
| DaFang-2 | | | | | | | 0 | 0 | 0 | 0 | 0 | 41537 | 258 | 0 | 0 | 11861 | 760 | 0 | | | | | |
| DaFang-8 | | | | | | | 0 | 0 | 0 | 0 | 0 | 352 | 17 | 0 | 0 | 1336 | 364 | 0 | | | | | |
| DaFang-9 | | | | | | | 0 | 0 | 0 | 0 | 0 | 2910 | 473 | 0 | 0 | 24021 | 603 | 0 | | | | | |
| DaFang-11 | | | | | | | 0 | 0 | 0 | 0 | 0 | 50 | 0 | 0 | 0 | 15191 | 71 | 0 | | | | | |
| DaFang-12 | | | | | | | 0 | 0 | 0 | 0 | 0 | 11437 | 102 | 0 | 0 | 5103 | 368 | 0 | | | | | |
| DaFang-10 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 80 | 0 | 0 | 910 | 582 | 0 | | | | | |
| DaFang-1 | | | | | | | 0 | 0 | 0 | 0 | 0 | 262 | 0 | 0 | 0 | 120 | 636 | 0 | | | | | |
| DaFang-2 | | | | | | | 0 | 0 | 0 | 0 | 0 | 5099 | 69 | 0 | 0 | 268 | 731 | 0 | | | | | |
| DaFang-3 | | | | | | | 0 | 0 | 0 | 0 | 0 | 3575 | 67 | 0 | 0 | 3598 | 764 | 0 | | | | | |
| DaFang-4 | | | | | | | 0 | 0 | 0 | 0 | 0 | 217 | 72 | 0 | 0 | 1090 | 645 | 0 | | | | | |
| DaFang-5 | | | | | | | 0 | 0 | 0 | 0 | 0 | 0 | 40 | 0 | 0 | 58 | 190 | 0 | | | | | |
| DaFang-6 | | | | | | | 0 | 0 | 0 | 0 | 0 | 1653 | 79 | 0 | 0 | 58 | 622 | 0 | | | | | |
| AS49 - 6 | | | | | | | wt | 0 | 0 | 0 | 0 | 6488 | 267 | 0 | 0 | 324 | 847 | 0 | | | | | |
| HCT-116 - 8 | | | | | | | wt | 0 | 0 | 0 | 0 | 209 | 0 | 0 | 0 | 34 | 573 | 0 | | | | | |
| HCT-116 - 8 | | | | | | | wt | 0 | 0 | 0 | 0 | 846 | 122 | 0 | 0 | 178 | 675 | 0 | | | | | |
| HT29 - 7 | | | | | | | mutant | 0 | 0 | 0 | 0 | 3501 | 0 | 0 | 0 | 855 | 844 | 0 | | | | | |
| HT29 - 7 | | | | | | | mutant | 0 | 0 | 0 | 0 | 3147 | 20 | 0 | 0 | 214 | 533 | 0 | | | | | |
| HT29 - 8 | | | | | | | mutant | 0 | 0 | 0 | 0 | 467 | 0 | 0 | 0 | 200 | 768 | 0 | | | | | |
| SF539 - 7 | | | | | | | wt | 0 | 0 | 0 | 0 | 375 | 55 | 0 | 0 | 21 | 624 | 0 | | | | | |
| SF539 - 8 | | | | | | | wt | 0 | 0 | 0 | 0 | 252 | 0 | 0 | 0 | 21 | 863 | 0 | | | | | |
| SF-206-7 | | | | | | | mutant | 0 | 0 | 0 | 0 | 446 | 164 | 0 | 0 | 706 | 659 | 0 | | | | | |
| SF-206-8 | | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 183 | 0 | 0 | 203 | 648 | 0 | | | | | |
| OVCAR-4 - 7 | | | | | | | wt | 0 | 0 | 0 | 0 | 1305 | 423 | 0 | 0 | 0 | 935 | 0 | | | | | |
| OVCAR-4 - 8 | | | | | | | wt | 0 | 0 | 0 | 0 | 527 | 339 | 0 | 0 | 2773 | 803 | 0 | | | | | |
| OVCAR-5 - 7 | | | | | | | mutant | 0 | 0 | 0 | 0 | 326 | 0 | 0 | 0 | 603 | 2164 | 0 | | | | | |
| OVCAR-5 - 8 | | | | | | | mutant | 0 | 0 | 0 | 0 | 0 | 315 | 0 | 0 | 511 | 556 | 0 | | | | | |
| MCF-7 - 8 | | | | | | | wt | 0 | 0 | 0 | 0 | 740 | 194 | 0 | 0 | 510 | 860 | 0 | | | | | |
| ADR-RES - 8 | | | | | | | mutant | 0 | 0 | 0 | 0 | 3013 | 0 | 0 | 0 | 296 | 1033 | 0</ | | | | | |

187
Table 3 (cont'd)

| Tissue | Tumor - sym | Normal - sym | Tumor - fa | Tumor cells | Normal | Endoc | p53 | SEC 116 | 2 |
|--------------------------------|-------------|--------------|------------|-------------|--------|-------|-----|---------|------|
| adrenal gland - h | | 1 | | | | | | | 94 |
| lymph node - h | | 2 | | | | | | | 834 |
| bone marrow - h | | 3 | | | | | | | 922 |
| mammary gland - h | | 4 | | | | | | | 0 |
| brain - h | | 5 | | | | | | | 2601 |
| pancreas - h | | 6 | | | | | | | 235 |
| carcinoma - h | | 7 | | | | | | | 680 |
| prostate gland - h | | 8 | | | | | | | 2327 |
| testis - h | | 9 | | | | | | | 2719 |
| total brain - h | | 10 | | | | | | | 1303 |
| placenta - h | | 11 | | | | | | | 717 |
| total kidney - h | | 12 | | | | | | | 762 |
| prostate - h | | 13 | | | | | | | 537 |
| total liver - h | | 14 | | | | | | | 548 |
| subcutaneous - h | | 15 | | | | | | | 410 |
| total lung - h | | 16 | | | | | | | 0 |
| skeletal muscle - h | | 17 | | | | | | | 154 |
| heart - h | | 18 | | | | | | | 514 |
| small intestine - h | | 19 | | | | | | | 282 |
| kidney - h | | 20 | | | | | | | 250 |
| apical cord - h | | 21 | | | | | | | 51 |
| liver - h | | 22 | | | | | | | 167 |
| Spleen - h | | 23 | | | | | | | 456 |
| lung - h | | 24 | | | | | | | 894 |
| stomach - h | | 25 | | | | | | | 60 |
| testis - h | | 26 | | | | | | | 141 |
| thyroid - h | | 27 | | | | | | | 332 |
| HPAEC | | 28 | | | | 28 | | | 0 |
| thyroid gland - h | | 29 | | | | | | | 168 |
| HPTEC | | 30 | | | | 30 | | | 3128 |
| trachea - h | | 31 | | | | | | | 91 |
| HPAEC | | 32 | | | | | | | 196 |
| uterus - h | | 33 | | | | | | | 160 |
| HCAEC | | 34 | | | | | | | 0 |
| Pancreas - h | | 35 | | | | | | | 170 |
| lymph node - h | | 36 | | | | | | | 71 |
| Skeletal muscle - h | | 37 | | | | | | | 1036 |
| total liver - h | | 38 | | | | | | | 102 |
| Heart - h | | 39 | | | | | | | 145 |
| thyroid - h | | 40 | | | | | | | 123 |
| Duodenum - h | | 41 | | | | | | | 537 |
| Fetal brain - h | | 42 | | | | | | | 140 |
| Subcutaneous - h | | 43 | | | | | | | 0 |
| testis - h | | 44 | | | | | | | 0 |
| HT21-normal | | | | | 365 | | | | 0 |
| HT21-normal | | | | | 363 | | | | 0 |
| HT157-normal | | | | | 356 | 356 | | | 1292 |
| Bas-13 | | | | | 354 | 354 | | | 1237 |
| Bas-12 | | | | | 344 | | | | 85 |
| carcinoma - h | | | | | 342 | | | | 0 |
| organ - h | | | | | 334 | 334 | | | 0 |
| HPTEC | | | | | 332 | | | | 139 |
| lymph node - h | | | | | 330 | | | | 141 |
| h adult SAMC 10/21/92 #17 | | | | | 328 | | | | 70 |
| Fetal brain - h | | | | | 327 | | | | 89 |
| HT208-normal | | | | | 326 | | | | 386 |
| thyroid - h | | | | | 321 | | | | 0 |
| HT143 - normal | | | | | 320 | | | | 0 |
| HEPM 3d untreated | | | | | 318 | | | | 148 |
| uterus - h | | | | | 316 | | | | 203 |
| trachea - h | | | | | 314 | | | | 173 |
| thyroid gland - h | | | | | 311 | | | | 0 |
| subcutaneous - h | | | | | 309 | | | | 66 |
| prostate - h | | | | | 307 | | | | 190 |
| prostate gland - h | | | | | 305 | | | | 0 |
| pancreas - h | | | | | 303 | | | | 0 |
| mammary gland - h | | | | | 302 | | | | 307 |
| kidney - h | | | | | 298 | | | | 16 |
| testis - h | | | | | 297 | | | | 60 |
| liver - h | | | | | 296 | | | | 21 |
| Spleen - h | | | | | 294 | | | | 111 |
| apical cord - h | | | | | 292 | | | | 0 |
| small intestine - h | | | | | 290 | | | | 0 |
| skeletal muscle - h | | | | | 279 | | | | 267 |
| bone marrow - h | | | | | 277 | | | | 136 |
| adrenal gland - h | | | | | 275 | 275 | | | 0 |
| HPAEC | | | | | 266 | | | | 0 |
| HT382-normal | | | | | 266 | | | | 88 |
| HT382-normal | | | | | 239 | 239 | | | 331 |
| Bas-11 | | | | | 235 | 235 | | | 222 |
| HT372-normal | | | | | 234 | | | | 0 |
| Bas-6 | | | | | 233 | 233 | | | 346 |
| Bas-7 | | | | | 231 | 231 | | | 467 |
| Bas-5 | | | | | 229 | 229 | | | 82 |
| Bas-3 | | | | | 227 | 227 | | | 442 |
| Bas-1 | | | | | 222 | | | | 80 |
| bladder - h | | | | | 215 | | | | 0 |
| Heart - h | | | | | 214 | | | | 1006 |
| stomach - h | | | | | 213 | | | | 0 |
| total liver - h | | | | | 212 | | | | 123 |
| placenta - h | | | | | 211 | 211 | | | 0 |
| HCAEC | | | | | 210 | | | | 0 |
| total brain - h | | | | | 209 | | | | 0 |
| HPAEC | | | | | 205 | | | | 267 |
| Duodenum - h | | | | | 203 | | | | 0 |
| Skeletal muscle - h | | | | | 201 | | | | 0 |
| Pancreas - h | | | | | 199 | | | | 0 |
| testis - h | | | | | 197 | | | | 0 |
| Subcutaneous - h | | | | | 195 | | | | 48 |
| HEPM 3d TGFB1 antagonist-DHase | | | | | 193 | | | | 0 |
| thyroid - h | | | | | 179 | | | | 0 |
| W138 T2n | | | | | 61 | | | | 0 |
| lymph node - h | | | | | 59 | | | | 0 |
| lung - h | | | | | 57 | | | | 0 |
| kidney - h | | | | | 55 | | | | 0 |
| Heart - h | | | | | 53 | | | | 0 |
| Fetal lung - h | | | | | 51 | | | | 36 |
| total liver - h | | | | | 49 | | | | 0 |
| total kidney - h | | | | | 79 | | | | 0 |
| HELA-2n-031899 | | | | | 81 | | | | 524 |
| HELA-0n-031899 | | | | | 83 | | | | 71 |
| HELA-0n-031899 | | | | | 86 | | | | 674 |
| HELA-0n-031899 | | | | | 88 | | | | 57 |
| HELA-0n-031899 | | | | | 90 | | | | 151 |
| HELA-0n-031899 | | | | | 92 | | | | 0 |
| HELA-10n-031899 | | | | | 94 | | | | 91 |
| HELA-11n-031899 | | | | | 96 | | | | 0 |
| HELA-12n-031899 | | | | | 146 | | | | 120 |
| NCH-M22N | | | | | 148 | | | | 9 |
| NCH-M460 | | | | | 150 | | | | 66 |
| NCH-M522 | | | | | 152 | | | | 294 |
| SAB-19 | | | | | 154 | | | | 0 |
| SAB-75 | | | | | 156 | | | | 137 |
| SF-268 | | | | | 158 | | | | 0 |
| SF-295 | | | | | 160 | | | | 165 |
| OCRP-CEM | | | | | 162 | | | | 0 |
| DL-145 | | | | | 164 | | | | 0 |
| HCT 116 | | | | | | | | | 0 |

Table 3¹⁸⁸
(cont'd)

| Tissue | Tumor sym | Normal sym | Tumor - 1e | Tumor cells | Normal | Endoc | p53 | SEQ 116 S |
|--------------------------------|-----------|------------|------------|-------------|--------|-------|-----|-----------|
| Cell-1 | | | | 162 | | | | 4 |
| F663 | | | | 163 | | | | 0 |
| T-47D | | | | 171 | | | | 72 |
| Kem-3 | | | | 181 | | | | 0 |
| CRB1441 RNA B/30 | | | | 183 | | | | 169 |
| 7817 untreated + DNase | | | | 194 | | | | 47 |
| K19 poly A+ | | | | 196 | | | | 0 |
| HOS poly A+ | | | | 198 | | | | 52 |
| ACHN | | | | 200 | | | | 0 |
| UACC-67 | | | | 202 | | | | 56 |
| MCF-7ADRES | | | | 204 | | | | 0 |
| UTOS (Mundy) poly A+ | | | | 206 | | | | 34 |
| WISH (Collagen) poly A+ | | | | 208 | | | | 200 |
| 458 muscle mRNA | | | | 218 | | | | 0 |
| COL137 RNA 3/21/88 | | | | 219 | | | | 0 |
| WL36 72h 0.5% FBS, 24h 10% FBS | | | | 220 | | | | 242 |
| CRB1441 + TPA (24h) B/30 | | | | 221 | | | | 60 |
| Kem-1 | | | | 222 | | | | 79 |
| Kem-2 | | | | 225 | | | | 0 |
| Kem-3 | | | | 241 | | | | 0 |
| HOP-82 | | | | 242 | | | | 0 |
| MOLT-4 | | | | 243 | | | | 0 |
| U937 | | | | 244 | | | | 0 |
| HL-60 | | | | 245 | | | | 0 |
| NCL-H23 | | | | 246 | | | | 60 |
| RPM8 8226 | | | | 247 | | | | 241 |
| ASWATCC | | | | 248 | | | | 0 |
| SR | | | | 249 | | | | 85 |
| OVCA-3 | | | | 250 | | | | 0 |
| MCT-15 | | | | 251 | | | | 0 |
| OVCA-4 | | | | 252 | | | | 0 |
| UEA-1 | | | | 253 | | | | 249 |
| OVCA-5 | | | | 254 | | | | 0 |
| SM12C | | | | 255 | | | | 0 |
| OVCA-8 | | | | 256 | | | | 0 |
| LOX MN | | | | 257 | | | | 0 |
| IGROV1 | | | | 258 | | | | 153 |
| SK-MEL-2 | | | | 259 | | | | 0 |
| SK-OV-3 | | | | 260 | | | | 0 |
| SK-MEL-5 | | | | 261 | | | | 0 |
| SP-539 | | | | 262 | | | | 0 |
| SK-MEL-28 | | | | 263 | | | | 72 |
| K-562 | | | | 264 | | | | 33 |
| UACC-257 | | | | 265 | | | | 0 |
| M14 | | | | 267 | | | | 49 |
| MCF7 | | | | 269 | | | | 169 |
| MDA-MB-435 | | | | 270 | | | | 0 |
| HT219 | | | | 271 | | | | 0 |
| MDA-N | | | | 272 | | | | 0 |
| Y78 poly A+ | | | | 289 | | | | 26 |
| KHOS poly A+ | | | | 300 | | | | 147 |
| HTB36 72h TPA RNA 6/73 | | | | 313 | | | | 83 |
| HELA-EXP-031029 | | | | 322 | | | | 0 |
| HTB36 0h RNA | | | | 323 | | | | 0 |
| HT37 | | | | 324 | | | | 125 |
| 458 muscle RNA | | | | 336 | | | | 0 |
| NCL-H26 | | | | 337 | | | | 0 |
| HOP-62 | | | | 338 | | | | 0 |
| MDA-MB-231 | | | | 339 | | | | 61 |
| U251 | | | | 340 | | | | 0 |
| PT cells poly A+ | | | | 341 | | | | 0 |
| PC-3 | | | | 343 | | | | 0 |
| HCC-2998 | | | | 345 | | | | 0 |
| SW-620 | | | | 346 | | | | 148 |
| HT192 | | | | 347 | | | | 0 |
| COLO 205 | | | | 348 | | | | 0 |
| HT218 | | | | 349 | | | | 0 |
| KM-12 | | | | 350 | | | | 20 |
| HT151 | | | | 351 | | | | 0 |
| A490 | | | | 352 | | | | 460 |
| HT393 | | | | 353 | | | | 0 |
| RJE 393 | | | | 355 | | | | 363 |
| TK-10 | | | | 357 | | | | 241 |
| Mdms-3M | | | | 359 | | | | 0 |
| Ms 5781 | | | 50 | | | | | 312 |
| HT213 | | | 52 | | | | | 0 |
| HT288 | | | 54 | | | | | 0 |
| HT139 | | | 56 | | | | | 0 |
| HT155 | | | 58 | | | | | 165 |
| HT163 | | | 60 | | | | | 61 |
| HT170 | | | 62 | | | | | 137 |
| HT172 | | | 63 | | | | | 0 |
| HT138 | | | 64 | | | | | 32 |
| HT178 | | | 65 | | | | | 19 |
| HT154 | | | 66 | | | | | 40 |
| HT180 | | | 67 | | | | | 140 |
| HT169 | | | 68 | | | | | 0 |
| HT185 | | | 69 | | | | | 0 |
| HT143 | | | 70 | | | | | 99 |
| HT190 | | | 71 | | | | | 130 |
| HT145 | | | 72 | | | | | 151 |
| HT227 | | | 73 | | | | | 0 |
| HT302 | | | 74 | | | | | 0 |
| HT314 | | | 76 | | | | | 0 |
| HT317 | | | 77 | | | | | 0 |
| Brachyothelasma 8425 11/8 | | | 78 | | | | | 21 |
| HT323 | | | 80 | | | | | 137 |
| HT327 | | | 82 | | | | | 0 |
| HT335 | | | 85 | | | | | 98 |
| HT146 | | | 87 | | | | | 29 |
| HT348 | | | 170 | | | | | 18 |
| HT311 | | | 185 | | | | | 0 |
| HT396 | | | 187 | | | | | 0 |
| HT140 | | | 189 | | | | | 205 |
| HT281 | | | 191 | | | | | 75 |
| HT372 | | | 207 | | | | | 40 |
| TCGP | | | 216 | | | | | 48 |
| HT160 | | | 217 | | | | | 67 |
| HT307 | | | 224 | | | | | 254 |
| HT368 | | | 226 | | | | | 0 |
| HT370 | | | 228 | | | | | 114 |
| HT371 | | | 230 | | | | | 125 |
| HT377 | | | 236 | | | | | 112 |
| HT382 | | | 281 | | | | | 468 |
| nanucll antisense RNA | | | 299 | | | | | 231 |
| HT334 | | | 301 | | | | | 0 |
| HT330 | | | 315 | | | | | 93 |
| HT302 | | | 317 | | | | | 0 |
| HT394 | | | 319 | | | | | 0 |
| HT312 | | | 325 | | | | | 0 |
| HT164 | | | 358 | | | | | 46 |
| HT395 | | | 360 | | | | | 13 |
| HT157 | | | | | | | | 63 |
| T-47D | 163 | | | | | | | 0 |
| MDA-N | 161 | | | | | | | 0 |
| MDA-MB-435 | 159 | | | | | | | 0 |
| MDA-MB-231 | 157 | | | | | | | 36 |

Table 3¹⁸⁹
(cont'd)

| Tissue | Tumor - ym | Normal - ym | Tumor - To | Tumor cells | Normal | Endoc | p53 | SEQ ID NO |
|-----------------------------|------------|-------------|------------|-------------|--------|-------|--------|-----------|
| HA5781 | 150 | | | | | | | 0 |
| MCF-7/ADR-RES | 153 | | | | | | | 0 |
| MCF7 | 151 | | | | | | | 0 |
| M14 | 145 | | | | | | | 0 |
| UACC-257 | 147 | | | | | | | 22 |
| UACC-62 | 145 | | | | | | | 0 |
| SK-MEL-28 | 144 | | | | | | | 33 |
| UO-31 | 143 | | | | | | | 0 |
| SK-MEL-5 | 142 | | | | | | | 91 |
| SK-M-12 | 141 | | | | | | | 4 |
| SK-MEL-2 | 140 | | | | | | | 263 |
| MCT-15 | 139 | | | | | | | 328 |
| Mamma-34 | 138 | | | | | | | 181 |
| CCLO-205 | 137 | | | | | | | 250 |
| LOX-B4V1 | 136 | | | | | | | 0 |
| SW-620 | 135 | | | | | | | 0 |
| TK-10 | 134 | | | | | | | 0 |
| MCT-116 | 133 | | | | | | | 0 |
| T86-0 | 132 | | | | | | | 82 |
| MCC-2998 | 131 | | | | | | | 76 |
| ACHN | 129 | | | | | | | 275 |
| PC-3 | 128 | | | | | | | 0 |
| RDX-393 | 128 | | | | | | | 336 |
| DLA-145 | 127 | | | | | | | 90 |
| C8a-1 | 126 | | | | | | | 276 |
| SF | 125 | | | | | | | 0 |
| A498 | 124 | | | | | | | 137 |
| RPMD B226 | 123 | | | | | | | 0 |
| SM12C | 122 | | | | | | | 126 |
| HE-40 | 121 | | | | | | | 0 |
| MOLT-4 | 120 | | | | | | | 118 |
| OVCAR-5 | 119 | | | | | | | 0 |
| K-562 | 118 | | | | | | | 38 |
| OVCAR-4 | 117 | | | | | | | 542 |
| QCRF-CEM | 116 | | | | | | | 806 |
| OVCAR-3 | 115 | | | | | | | 161 |
| SF-639 | 114 | | | | | | | 87 |
| HOP-62 | 113 | | | | | | | 0 |
| SF-275 | 112 | | | | | | | 161 |
| ASMBATCC | 111 | | | | | | | 110 |
| SF-268 | 110 | | | | | | | 133 |
| NCL-H522 | 109 | | | | | | | 0 |
| U251 | 108 | | | | | | | 204 |
| NCL-H460 | 107 | | | | | | | 0 |
| SMB-75 | 106 | | | | | | | 38 |
| NCL-H522M | 105 | | | | | | | 430 |
| SMB-19 | 104 | | | | | | | 78 |
| NCL-H26 | 103 | | | | | | | 62 |
| SK-OV-3 | 102 | | | | | | | 6 |
| NCL-H23 | 101 | | | | | | | 777 |
| OROV1 | 100 | | | | | | | 0 |
| EKX2 | 99 | | | | | | | 54 |
| OVCAR-8 | 98 | | | | | | | 0 |
| HOP-92 | 97 | | | | | | | 43 |
| n. keratinase 3/11/92 #12 | 48 | | | | | | | 148 |
| n. adu. SAMC 10/21/92 #17 | 47 | | | | | | | 210 |
| n. keratinocyte 2/25/92 #10 | 46 | | | | | | | 135 |
| TCCP | 26 | | | | | | | 0 |
| AS49-1 | | | | | | | wt | 5 |
| AS49-3 | | | | | | | wt | 379 |
| AS49-4 | | | | | | | wt | 458 |
| AS49-5 | | | | | | | wt | 347 |
| AS49-7 | | | | | | | wt | 73 |
| EKXV-1 | | | | | | | mutant | 84 |
| EKXV-4 | | | | | | | mutant | 290 |
| EKXV-3 | | | | | | | mutant | 0 |
| EKXV-5 | | | | | | | mutant | 443 |
| EKXV-7 | | | | | | | mutant | 877 |
| MCF-7-1 | | | | | | | wt | 0 |
| MCF-7-3 | | | | | | | wt | 565 |
| MCF-7-4 | | | | | | | wt | 315 |
| MCF-7-5 | | | | | | | wt | 0 |
| MCF-7-7 | | | | | | | wt | 0 |
| ADR-RES-1 | | | | | | | mutant | 3049 |
| ADR-RES-3 | | | | | | | mutant | 158 |
| ADR-RES-4 | | | | | | | mutant | 79 |
| ADR-RES-5 | | | | | | | mutant | 18 |
| ADR-RES-7 | | | | | | | mutant | 96 |
| WI-38-1 | | | | | | | wt | 0 |
| WI-38-3 | | | | | | | wt | 283 |
| WI-38-4 | | | | | | | wt | 560 |
| WI-38-5 | | | | | | | wt | 589 |
| WI-38-7 | | | | | | | wt | 0 |
| HuLa-1 | | | | | | | HPV E6 | 0 |
| HuLa-3 | | | | | | | HPV E6 | 56 |
| HuLa-4 | | | | | | | HPV E6 | 185 |
| HuLa-5 | | | | | | | HPV E6 | 308 |
| HuLa-7 | | | | | | | HPV E6 | 105 |
| H1299-1 | | | | | | | mutant | 0 |
| H1299-3 | | | | | | | mutant | 0 |
| H1299-4 | | | | | | | mutant | 0 |
| H1299-5 | | | | | | | mutant | 0 |
| H1299-7 | | | | | | | mutant | 1 |
| AS49-2 | | | | | | | wt | 183 |
| EKXV-2 | | | | | | | mutant | 0 |
| HCT-116-1 | | | | | | | wt | 0 |
| HCT-116-2 | | | | | | | wt | 820 |
| HT29-7 | | | | | | | mutant | 68 |
| SF530-1 | | | | | | | wt | 0 |
| SF530-2 | | | | | | | wt | 3 |
| SF-268-1 | | | | | | | mutant | 209 |
| SF-268-2 | | | | | | | mutant | 631 |
| OVCAR-4-1 | | | | | | | wt | 0 |
| OVCAR-4-2 | | | | | | | wt | 0 |
| OVCAR-5-1 | | | | | | | mutant | 523 |
| OVCAR-5-2 | | | | | | | mutant | 208 |
| MCF-7-2 | | | | | | | wt | 86 |
| ADR-RES-2 | | | | | | | mutant | 221 |
| HuLa-2 | | | | | | | HPV E6 | 173 |
| SW480-1 | | | | | | | mutant | 0 |
| SW480-2 | | | | | | | mutant | 191 |
| H1299-2 | | | | | | | mutant | 1003 |
| C33A-1 | | | | | | | mutant | 0 |
| C33A-2 | | | | | | | mutant | 0 |
| U2OS-1 | | | | | | | mutant | 211 |
| U2OS-2 | | | | | | | mutant | 557 |
| Hu68-1 | | | | | | | wt | 0 |
| Hu68-2 | | | | | | | wt | 24 |
| WI-38-2 | | | | | | | wt | 299 |
| Madar-1 | | | | | | | wt | 0 |
| Madar-2 | | | | | | | wt | 0 |
| Madar-3 | | | | | | | wt | 0 |
| Madar-4 | | | | | | | wt | 14320 |
| Madar-5 | | | | | | | wt | 552 |
| Madar-6 | | | | | | | wt | 0 |
| Madar-8 | | | | | | | wt | 0 |
| Madar-9 | | | | | | | wt | 0 |

190
Table 3 (cont'd)

| Tissue | Tumor - ym | Normal - ym | Tumor - to | Tumor cells | Normal | Endos | p53 | SEO 116 3 |
|-----------------------------|------------|-------------|------------|-------------|--------|-------|--------|-----------|
| DeFang-2 | | | | | | | | 1582 |
| DeFang-6 | | | | | | | | 2991 |
| DeFang-9 | | | | | | | | 603 |
| DeFang-11 | | | | | | | | 2503 |
| DeFang-12 | | | | | | | | 518 |
| DeFang-10 | | | | | | | | 368 |
| DeFang-1 | | | | | | | | 474 |
| DeFang-3 | | | | | | | | 0 |
| DeFang-2 | | | | | | | | 222 |
| DeFang-4 | | | | | | | | 0 |
| DeFang-5 | | | | | | | | 0 |
| DeFang-6 | | | | | | | | 0 |
| AS49 - 6 | | | | | | | wt | 0 |
| EVX - 8 | | | | | | | mutant | 56 |
| HCT-116 - 7 | | | | | | | wt | 0 |
| HCT-116 - 8 | | | | | | | wt | 0 |
| HT29 - 1 | | | | | | | mutant | 310 |
| HT29 - 7 | | | | | | | mutant | 69 |
| HT29 - 9 | | | | | | | mutant | 0 |
| SF539 - 7 | | | | | | | wt | 155 |
| SF539 - 8 | | | | | | | wt | 259 |
| SF-268-7 | | | | | | | mutant | 218 |
| SF-268-8 | | | | | | | mutant | 501 |
| OVCAR-4 - 7 | | | | | | | wt | 405 |
| OVCAR-4 - 8 | | | | | | | wt | 0 |
| OVCAR-5 - 7 | | | | | | | mutant | 631 |
| OVCAR-5 - 8 | | | | | | | mutant | 107 |
| HCT-7 - 8 | | | | | | | wt | 35 |
| ADR-RES - 8 | | | | | | | mutant | 857 |
| Hae-8 - 8 | | | | | | | HPV E6 | 0 |
| SW480 - 7 | | | | | | | mutant | 0 |
| SW480 - 8 | | | | | | | mutant | 0 |
| HT299 - 8 | | | | | | | mutant | 0 |
| C33A - 7 | | | | | | | mutant | 0 |
| C33A - 8 | | | | | | | mutant | 0 |
| U2OS - 7 | | | | | | | mutant | 729 |
| U2OS - 8 | | | | | | | mutant | 37 |
| Hae8 - 7 | | | | | | | wt | 0 |
| Hae8 - 8 | | | | | | | wt | 0 |
| WI 38 - 8 | | | | | | | wt | 0 |
| 4.58 methyl RNA | | | | | | | wt | 0 |
| CRL 1572 3/17/89 | | | | | | | | 71 |
| Bev-4 | | | | | | 84 | | 221 |
| HT368 | | | | | | | | 80 |
| HT378 | | | | | | | | 151 |
| HT385 | | | | | | | | 80 |
| HT309 | | | | | | | | 0 |
| Bev-3 | | | | | | 173 | | 487 |
| Bev-5 | | | | | | 175 | | 117 |
| Bev-9 | | | | | | 177 | | 481 |
| In test atrophy 2/25/92 #10 | | | | | | | | 0 |
| Bev-10 | | | | | | 237 | | 0 |
| HTB10 | | | | | | | | 0 |
| In fibroblasts 3/31/92 #12 | | | | | | | | 0 |
| prostate h | | | | | | | | 0 |
| huvng-O5 poly A+ | | | | | | | | 32 |
| SA-O5 (huvng) poly A+ | | | | | | | | 0 |
| huc poly A+ | | | | | | | | 0 |
| HCT-116 - 3 | | | | | | | wt | 384 |
| HCT-116 - 4 | | | | | | | wt | 0 |
| HCT-116 - 5 | | | | | | | wt | 0 |
| HCT-116 - 6 | | | | | | | wt | 0 |
| AS49 - 6 | | | | | | | wt | 0 |
| HT29 - 3 | | | | | | | mutant | 874 |
| EVX - 6 | | | | | | | mutant | 121 |
| HT29 - 4 | | | | | | | mutant | 540 |
| HT29 - 5 | | | | | | | mutant | 0 |
| HT29 - 6 | | | | | | | mutant | 171 |
| OVCAR-4 - 3 | | | | | | | wt | 339 |
| OVCAR-4 - 4 | | | | | | | wt | 0 |
| OVCAR-4 - 5 | | | | | | | wt | 16 |
| OVCAR-4 - 6 | | | | | | | wt | 0 |
| SF539 - 3 | | | | | | | wt | 726 |
| SF539 - 4 | | | | | | | wt | 83 |
| SF539 - 5 | | | | | | | wt | 0 |
| SF539 - 6 | | | | | | | wt | 0 |
| OVCAR-5 - 3 | | | | | | | mutant | 2219 |
| OVCAR-5 - 4 | | | | | | | mutant | 266 |
| OVCAR-5 - 6 | | | | | | | mutant | 0 |
| ADR-RES - 6 | | | | | | | mutant | 0 |
| HCT-7 - 9 | | | | | | | wt | 279 |
| Hae-8 - 6 | | | | | | | HPV E6 | 371 |
| HT299 - 6 | | | | | | | mutant | 0 |
| SW480 - 3 | | | | | | | mutant | 51 |
| SW480 - 4 | | | | | | | mutant | 0 |
| SW480 - 5 | | | | | | | mutant | 293 |
| SW480 - 6 | | | | | | | mutant | 225 |
| C33A - 3 | | | | | | | mutant | 173 |
| C33A - 4 | | | | | | | mutant | 162 |
| C33A - 5 | | | | | | | mutant | 0 |
| C33A - 6 | | | | | | | mutant | 55 |
| Hae8 - 6 | | | | | | | wt | 0 |
| U2OS - 3 | | | | | | | mutant | 620 |
| U2OS - 4 | | | | | | | mutant | 561 |
| U2OS - 5 | | | | | | | mutant | 644 |
| U2OS - 6 | | | | | | | mutant | 0 |
| WI 38 - 6 | | | | | | | wt | 0 |
| Hae8 - 3 | | | | | | | wt | 288 |
| Hae8 - 4 | | | | | | | wt | 821 |
| SF-268-3 | | | | | | | mutant | 277 |
| SF-268-4 | | | | | | | mutant | 0 |
| SF-268-5 | | | | | | | mutant | 125 |
| SF-268-6 | | | | | | | mutant | 33 |
| DeFang-13 | | | | | | | | 21 |
| Michal - 20 | | | | | | | | 368 |
| Michal - 21 | | | | | | | | 0 |
| Michal - 22 | | | | | | | | 0 |
| OVCAR-6 - 5 | | | | | | | mutant | 611 |
| Michal - 10 | | | | | | | | 96 |
| Michal - 11 | | | | | | | | 299 |
| Michal - 12 | | | | | | | | 684 |
| Michal - 13 | | | | | | | | 309 |
| Michal - 14 | | | | | | | | 150 |
| Michal - 15 | | | | | | | | 332 |
| Michal - 16 | | | | | | | | 0 |
| Michal - 17 | | | | | | | | 129 |
| Michal - 18 | | | | | | | | 0 |
| Michal - 19 | | | | | | | | 173 |

Table 4

| Gene Name | SP ID# | na ID# | aa | Family | Group | Length | AA | Extra-Catalytic Domains (Amino acid positions) |
|----------------------|--------|--------|-----|--------|----------|--------|----|---|
| X69117_h_beta_adrend | H | 1 | 122 | AGC | GRK | 688 | | Regulator of G-protein signaling domain 54-175; PH domain 559-652 |
| AA144574_m | M | 2 | 123 | AGC | GRK | 378 | | PH domain 249-337 |
| AA210825_h | H | 9 | 130 | AGC | PKC | 978 | | Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577 |
| AA316804_h | H | 11 | 132 | AGC | PKC | 890 | | Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532 |
| AA887783_h | H | 21 | 142 | AGC | SGK | 446 | | PX domain 13-120 |
| AA021445_h3 | H | 32 | 152 | CAMK | EMK | 1311 | | Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain 1072-1113 |
| R31237_1_h_AAC3348 | H | 34 | 154 | CAMK | EMK | 729 | | UBA domain 327-365 |
| 4067865_h | H | 36 | 156 | CAMK | EMK | 1330 | | PAS domain 133-186, 247-280, 354-386 |
| Z36720_h | H | 41 | 161 | CAMK | MLCK | 874 | | WD domain, G-beta repeat 674-711 |
| SGK088_h | H | 42 | 162 | CAMK | Trio | 2287 | | Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-390, 1697-1779 |
| R19772_h | H | 44 | 164 | CAMK | Trio | 1287 | | RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain 419-528 |
| 17000139801197_h_IRA | H | 76 | 195 | Other | IRAK | 596 | | Death domain 26-106 |
| AA088547_h | H | 78 | 197 | Other | IRE | 922 | | POQ enzyme repeat 39-76 |
| AA232253_h | H | 82 | 201 | Other | MLK | 800 | | SAM domain (Sterile alpha motif) 337-408 |
| AA599286_h | H | 89 | 208 | Other | SLOB | 649 | | PX domain 16-122 |
| AA836348_h | H | 113 | 232 | STE | NEK | 836 | | Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650 |
| PAK6_h | H | 115 | 234 | STE | STE20-02 | 719 | | P21-Rho-binding domain 11-69 |

FIGURE 1A

SEQ ID NO: 122_X69117_H BARK2_H
MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN
QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC
SHPFSKQAVEHVQSHLSKKQVTSTLFQOPYIEEICESLRGDI FQKFMESDKFTRFCQWKNV
ELNIHLTMNEFSVHRI IGRGGFGEVYGCRKADTGKMYAMKCLDKKRI KMKQGETLALNER
IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVPSEKEMRFYATE
I I L G L E H V H N R F V V Y R D L K P A N I L L D E H G H A R I S D L G L A C D F S K K K P H A S V G T H G Y M A P E
V L Q K G T A Y D S S A D W F S L G C M L F K L L R G H S P F R Q H K T K D K H E I D R M T L T V N V E L P D T F S P E
L K S L L E G L L Q R D V S K R L G C H G G G S Q E V K E H S F F K G V D W Q H V Y L Q K Y P P L I P P R G E V N A A
D A F D I G S F D E E D T K G I K L L D C D Q E L Y K N F P L V I S E R W Q Q E V T E T V Y E A V N A D T D K I E A R K
R A K N K Q L G H E E D Y A L G K D C I M H G Y M L K L G N P F L T Q W Q R R Y F Y L F P N R L E W R G E G E S R Q N L
L T M E Q I L S V E E T Q I K D K K C I L F R I K G G K Q F V L Q C E S D P E F V Q W K K E L N E T F K E A Q R L L R R
A P K F L N K P R S G T V E L P K P S L C H R N S N G L

SEQ ID NO: 123_AA144574_M BARK2_M
CFVVYRDLKPANILLDEYGHVRI SDLGLACDFS KKKPHASVGTHGYMAPEVLQKGTCYDS
SADWFSLGCMFLKLLRGHSPFRQHKT KD KHEIDRMTLT VNVQLPDAFSPELRSLLEGLLQ
RDVSQRLGCGGGGARELKEHIFFKGIDWQH VYLRKYPPPLI PPRGEVNAA DAFDIGSFDE
EDTKGI KLLDCDQDLYKNFPLV I SERWQQEVVETIYDAVNADTDKIEARKKAKNKQLGQE
EDYAMGKDCIMHGYMLKLG NPF LTQWQRRYFYLF PNRLEWRGEGESRQSLLTMEQIMSVE
ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLRRAPKFLNKPRA
AILEFSKPPLCHRNSSGL

SEQ ID NO: 124_AA826850_H
MGSSMSAATARRPVFDDKEDVNFDFHFI LRAIGKGSFGKVCIVQKRDT EKMYAMKYMKNQ
QCIERDEVNRN VFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ
FSEDTVRLYICEMALALDYL RGQHI IHRDVKPDNILLDERGHAHLTDFNIATIIK DGERA
TALAGTKPYMAPEIFXSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLV
QLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVE
PGFVPNKGR LHCDPTFELEEMILES RPLHKKKKRLAKNKS RDNSRDSSQSENDYLQDCLD
AIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMC GPICPSAGSG

SEQ ID NO: 125_AA960957_H
MGGNHSKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMKNQKCI
ERDEVNRN VFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE
GTVKLYICELALALEYLQRYHI IHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM
AGTKPYMAPEVFQVYMDRGP GYSYPVDWWSLGITAYELLRGWRPYEIH SVTPIDEILNMF
KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWD AVFKKALMPGF
VPNKGR LNCDPTFELEEMILES KPLHKKKKRLAKNRSRDGT KDSCPLNGHLQH CLETVRE
EFIIFNREKLRRQQGQGSQLLD TDSRGGGQAQSKLQDGCNNNLLTHTCTRGCSS

SEQ ID NO: 126_TBK1_H
MQSTSNHLWLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK
KLNHKNI VKLFAIEEETTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV
GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVS LYGTEEYL
HPDMYERAVLRKDHQKKYGATVDLWSIGVT FYHAATGSLPFRPFEGPRRNKEVMYKIITG
KPSGAISGVQKAENGPI DWSGDMPVSCSLSRGLQVLLTPVLANI LEADQEKCWGFDQFFA
ETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHEL VYKQTKI ISSNQELIYEGRRLV
LEPGRLAQHF PKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDL DGDASMAKAITG
VVCYACRIASTLLLYQELMRKGIRWLI ELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

1/115

FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE
GTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMD
GGLRNVDCCL

SEQ ID NO: 127_AA305176_H
MDPTAGSKKEPGGGAATEEGVNRIVPKPPSIEEFSIVKPISRGAFGKVYLGQKGGKLYA
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIIGDVK
LLHIYGYFDEEMAVKYISEVALALDYLHRHGI IHRDLKPDNMLISNEGHIKLTDFGLSKV
TLNRDINMMDILTTPSMAKPRQDYSRTPGQVLSLSSLGFNTPIAEKNQDPANILSACLS
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128_AA116841_M
TRPIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV
PQPDDETDTSYFEARNNAQHLLTVSGFSL

SEQ ID NO: 129_AA256100_H
MAMTAGTTTTFPMNSHTRERVTVAKLTLENFYSNLILQHEERETROKKLEVAMEEEGLAD
EEKKLRRSQHARKETEFRLRLKRTRLGLDDFESLKVIGRGAFGEVRLVQKKDTGHIYAMKI
LRKSDMLEKEQVAHIRAERDILVEADGAWVVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM
KKDTLTTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLLDAGHVKLSDFGGLCTGLKK
AHRTEFYRNLTHNPPSDFSFQNMNSKRKAETWKKNRRQLAYSTVGTDPDYIAPEVFMQTGY
NKLCDWWSLGVIMYEMLI GYPPFCSETPQETRYKVMNWKETLVFPPEVPISEKAKDLILR
FCIDSENRI GNSGVEEIKGHPFFEGVDWEHIRERPAAPIEIKSIDDTSNFDDFPESDIL
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQRGSIPTYMKAGKL

SEQ ID NO: 130_AA210825_H
DSLLPTPALGTPLPIPWVPGSLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG
SPLSHLLTRSRGSRTQGPPGPGGSRVGSRRVPGLPWP PPPHYPAGLPGPSPGPSPP
PPGGLELQSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVQLACSIVDQKF
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVLSASATFEDFQIRPHAL
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLNHYHKRCAFSIPNNCSGARKRRLSSTSL
ASGHSVRLGTSES L PCTAEELSRTTELLPRRPPSSSSSSSASSYTGRPIELDKMLLSKV
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDKFNCHKRCATRVPNDCLEALIN
GDVPMEEATDFSEADKSALMDESEDSGVI PGSHSENALHASEEEEEGEGGKAQSSLGYIPL
MRVVQSVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITL FQNNTTNRYEKEI
PLSEILTVE SAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGTGGPSGQGAEAARGLX
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG
QFGVVYGGKHKRTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLRHPGIVNLECMFETP
EKVFVVMKELHGDMLEMILSSEKGR LPERLTKFLITQILVALRHLHFKNIVHCDLKPENV
LLASADFPQVKLCDFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVGVI
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASPW SHISAGAILNNLLQVKMRKRYSDVK
SLSHPWLQEQYQTWLDLRELEGKMGERYITHESDDARWEQFAAEHPLPGSGLP TDRDLGGA
CPPQDHDMQGLAERISVL

SEQ ID NO: 131_AA127299_H
IQFIIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKKTLTPTWNETFFVHFPEKTTLEL
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

2/113

FIGURE 1C

SEQ ID NO: 132_AA316804_H

MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV
SFLQLIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN
ILQLITSADIEHEGDLVEVVLALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR
QGLKCEGCGLNHYHKRCAPFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES
HVHQEPSKRIPSWSGRPIWMEKMMVCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINDSSRGLDDT
EESPPEDEKMFFLDPSDLDERDEEAVKTISPSTSNNIPLMRVVQSIKHTKRKSSTMVKE
GWMVHYTSRDNLRKRHYWRLLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG
SNPHCFEIIITDMVYFVGENNGDSSHPVLAATGVGLDVAQSWEKAIRQALMPVTPQASV
CTSPGQGDHKLSTSI SVSNCQIQENVDISTVYQIFADEVLGSGQFGIVYGGKHKRKTGR
DVAIKVIDKMRFPKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVMEKLHGDML
EMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEFPQVKLCD
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSGYNRSLDMWSVGVIIVVSLSGTFPFNEDE
DINDQIQNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSDKSLSHPLQDYQTWLD
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133_PKNBETA_H

MEEGAPRQPGPSQWPPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHLGHVQQLLRSS
NRRLEQLHGELRELHARILLPGPGPGAEPVASGPRPWAEQLRARHLEALRRQLHVELKV
KQGAENMTHTCASGTPKERKLLAAQQMLRDSQLKVALLRMKISSLEASGSPEPGPELLA
EELQHRHLHVEAAVAEGAKNVVLLSSRRTQDRKALAEAAQQLQESSQKDLLRLALEQLL
EQLPPAHLPLRSRVTRRELRAAVPGYPQPSGTPVKPTALTGTQLQVRLLGCEQLLTAVPGRSP
AAALASSPSEGWLRTKAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI
PLERARELEIGVHWRDWRQLCGVAFLRLEDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSPSTISPPKGCPRTR
PTTLREASDPATPSNFLPKKTPPLGEEMTPPKPPRLYLPQEPTSEETPRTRKPHMEPRTR
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLLVQFKGTGKYAIAKALKKQEVLSRDE
IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSHARFVTEFVPGGDLMMQIHEDVFPEPQ
ARFYVACVVLGLQFLHEKKIIYRDLKLDNLLLDAAQGLFKIADFGLCKEGIGFGDRTSTFC
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPG
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLC
GPADLRYFEGEFTGLPPALTPPAPHSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 134_AI021023_M PKNBETA_M

LKWDNLLLLDAQGFLKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG
LGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA
GEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTPPAP
HSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 135_H19102_H

GGNIRGPWARGWKS LWTGLGTIRSDLEELWELRGHHYHQLHESLKPAVPLVEKPLPEWPVP
QFINLFLPEFPPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVVLQR
DTVRQCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYCSTDLYSLWSAVGCFPEASI
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHSVAMLASVTHSDSEIPAS
LNQGLSLLLHELLCQNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS
SAETMPFDDFDCDLESFLLYPIPA

3/113

FIGURE 1D

SEQ ID NO: 136_AA476563_H

MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFFTLPDGDSASRSFNTSESKVEFKAQ
DTISRGSDSVPVVISFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN
IGIIENKLLEAPDVLCLRLSTEQCQAHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF
VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTESLFRICSPLSGANEYIASTDT
LKTEEVLLFTDQTDLLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS
CSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP
ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPPFFTPVDWAEELMR

SEQ ID NO: 137_AA626690_H

MLPFAPQDEPWREMEVFSGGGASSGEVNLKMOVDEPMEEGEADSCHDEGVVKEIPITHH
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT
KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTTEEDVKFYLA
ELALALDHLHLQGLIVYRDLKPENILLDEIGHIKLTDFGLSKESVDQEKKAYSFCGTVEYM
APEVVNRRGHSQSADWWSYGVLMFEMLTGTLPFQGKDRNETMNMILKAKLGMPQFLSAEA
QSLRLMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDDTFCF
DPEFTAKTPKDSPGLPASANAHQLFKGFSFVATSIAEEYKITPITSANVLPVQINGNAA
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI
ITLKDVFDDGRYVYLVTDLMKGGELLDRILKQKCFSEEREASDILYVISKTVDYLHCQGVV
HRDLKPSNIIYMDSESASADSIRICDFGFAKQLRGENGILLTPCYTANFVAPEVLMQQGYD
AACDIWSLGLVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ
PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138_AA215680_H

MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVDPDMTKRDYLVDAATQIRLA
LERDVSEDYEAAFNHYQNGVDVLLRGIHVDPNKERREAVKLKITYLRRAEIEFNCHLQR
PLSSGASPSAGFSSLRLRPRTLSSAVEQLRGCRVVGVIKVLVQDPATGGTFVVKSLP
RCHMVSRLRTIIPHGVPMYTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL
SSGSTQERMKAQLNPHLNLTPARLPSPGHAPGQDRIALEPPRTSPNLLLAGEAPSTRPQR
EAEGEPTARTSTSGSSDLPKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG
RGMDQSCLSDAGAGRGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL
DQAGHIRLTYFGQWSEVEPQCCGEAVDNLISAPEVGGISELTEACDWWSFGLLYELLTG
MALSQSHPSGIQAHTQLQLPEWLSRPAASLLTELLQFEPTRRLLGMGEGGVSKLKSHPPFS
TIQWSKLVG

SEQ ID NO: 139_SGK_H

MTVKTEAAKGTLYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKI
SQPQEPPELMNANPSPPPSPSQQINLGPSSNPFAKPSDFHFLKVIKGSFGKVLLARHKA
EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYR
NTAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW
DDLINKKITPPFNPVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG
FSYAPPTDSFL

SEQ ID NO: 140_AA107515_M

MTVKAEAAARSTLYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM
SHPQEPPELMNANPSPPPSPSQQINLGPSSNPFAKPSDFHFLKVIKGSFGKVLLARHKA

FIGURE 1E

EVFYAVKVLQKKAILKKKEEKHIMSEENVLLKNVKNHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN
TAEMYDNI LNKPLQLKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD
DLINKKITPPFNPVSGPSDLRHFDPEFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF
SYAPPVDSFL

SEQ ID NO: 141_AA109508_M

HLQRRERFLEPRARFYAAEVASAI GYLHSLNII YRDLKPENILLDCQGHVVLTD FGLCKE
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVVSQMY
ENILHQPLQIPGGRTVAACDLLQSL LHKDQRQRLGSKADFLEIKNHVFFSPINWDDLYHK
RLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD
ILDC

SEQ ID NO: 142_AA887783_H

MQRDHTMDYKESCPVXIPSSDEHREKKKRFTVYKVLVSVGRSEWFVFRRYAEFDKLYNT
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMD
SPKHQSDPSEDEDERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKVLLAK
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKNHPFLVGLHYFSFQTEKLYFVL
DFVNGGEGHVVLTD FGLCKEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAV
LYEMLYGLPPFYCRDVAEMYDNI LHKPLSLRPGVSLTAWSI LEELEKDRQNRLGAKEDF
LEIQNHPPFFESLSWADLVQKKIPPPFNPVNAVGPDDIRNFDTAFTEETVPYSVCVSSDYSI
VNASVLEADDAFVGFSYAPPSEDLFL

SEQ ID NO: 143_R47805_H

MAHQGTGIHATEELKEFFAKARAGSVRLIKVVI EDEQLVLGASQEPVGRWDQDYDRAVLPL
LDAQQPCYLLYRLDSQNAQGF EWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDE
LFGTVKDDL SFAGYQKHLSSCAAPL TSAERELQQIRINEVKTEI SVESKHQTLQGLAF
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL
YKHTHEGDPLESVVFIIYSMPGYKCSI KERMLYSSCKSRL LDSVEQDFHLEIAKKIEIGDG
AELTAEFLYDEVHPKQHAFAKQAFAPKPGPGGRGHRKRLIRGPGENGDDS

SEQ ID NO: 144_H60215_H

MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR
KDGTDDFYQLKILTLEERGDQGI ESQEERQGMLLHTEYSLLSLLHTQDGVVHHHGLFQD
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFS DKTADLINLQHVIKEKRLSERETV
VIFYDVVRVVEALHQKNIVHRDLKLGNMVNLKRTHRITITNFC LGKHLVSEGDLLKDQRG
SPAYISPDVLSGRPYRGKPSDMWALGVVLF TMLYGQFPFYDSIPQELFRKIKAAEYTIPE
DGRVSENTVCLIRKLLVLDPQQR LAAADVLEALS AIIASWQSLSSLSGPLQVVPDIDDQM
SNADSSQEAKVTEEC SQYEFENYMRQQLLLAEKSSI HDTRSWVPKRQFGSAPPVRLGH
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145_SGK324_H

MASTRSIELEHFEERDKRPRPGSRRGAPSSSSGGSSSSSGPKGNGLIPSPAHSAHCSFYRTR
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGTSRALAAA
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLT DITEAIKXASG
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS
RSSAVKYSGSKSPGPSRRSQISAHGRSSSNVNGGP ELDRCSPEGVNGNRCSESSTLLEK
YKIGKVI GDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

5/118

FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH
RDIKPENLLVCEYPDGTKSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD
IWAAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ
VNVEARCTAGQILSHPWVSDDASQENNMQA EVTGKLGKQHFNNALPKQNSTTTGVSVMVS
GRRQVWPDCGAGLEVFELGSRELPSHGSWCLP

SEQ ID NO: 146_W30246_M SGK324_M
TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPEGVNGNRCSESFPLLEKYR
IGKVI GDGNFAVVKECVD RYTGKEFALKI IDKAKCCGKEHLIENEVSILRRVKHPNIIML
VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHSLSIVHRD
IKPENLLVCEYPDGTKSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW
AAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147_AA383293_H
PAAKRVVYRNGDPFFPGSQLVVTQRRFPTMEAFLEVTSAVQAPLAVRALYTPCHGHPV
TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPFSLKLSQAASQDWETVL
KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPPALSTRGLLAA
GNEAHLRSGVGT VAGSPKPLGRKAKKETCLIVTLTKYQQSETSRDGQSFP SGVIGVYGA
PHRRKETAGALEVADDED TQTEEP LDQRAAQIVEQVTC LQDFFGDDDFIACGPEKFRYA
QDDFVL DHSRRLLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGGRMTLRDDQPAKLEK
EPKTRPEENKPERPSGRKPRPMGI IAA NVEKHYETGRVIGDGNFAVVKECRHRETRQAYA
MKIIDKSRLKKGEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI
IESVKFPEPDAA LMIMDLCKALVHMHDKSI VHRDLKPENLLVQRNEDKSTTLKLADFGLA
KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPXXGDQDE
LFNIIQLGHFEFLPPYWDNISDAAKDLVSRLLVVDPKKRYTAHQVLQHPWIE TAGKTNTV
KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148_AA197883_M
MPTAPVLRPPPPPATPAPPAPSRPAPPPIPGHRGPCDHSLKCLSSKISERKLPGPWLPAGR
GPLEKPVLGPRGAVMPLFSPQSSLHSVRAEHSPLKPRVVTVVKLGGQPLRKATLLLNRRS
VQTFEQLLSDI SEALGFPRWKNDVRKLF TLKGREVKSVSDFFREGDAFIAMGKEPLTLK
SIQLAMEELYPKNRALALAPHSRVSPRLRSRLPSKLLKGSHRCGEAGSYSAEMESKAVS
RHQGTSTVLAPEDKARAQKWVRGKQSESEPGPPSPGAATQEETHASGEKHLGVEIEKTS
GEIVRCEKCKRERELQLGLQREPCPLGTSEL DLGRAQKRDSEKLVRTKSCRPSKAKFTD
GEEGWKGD SHRGSPRDP PQEMRRPNSNSDKKEIRGSESQDSYPQGAPKAQKDFVEGPPAV
EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPQLPRTRGEEKQAEHEKKPGGLGERRAPE
KESKRKLEEKRPERPSGRKPRPKGII SADVEKHYDIGGVIGDGNFATVKECRHRETRQAY
AMKMIDKSQLKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA
IVENVKFPEPEAAVMITDLCKAFVHMHDKNI VHRDVKPENLLVQRNEDKSI TLKLADFG
AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPERDQDE
LFNIIQVGQFEFLSPYWDNISDAAKDLVRNLLVDPKKRYTAEQVLQHPWIE MVGHTNTG
NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149_DRAK2_H
MSRRRFDCRSISGLLTTPQIP IKMENFNNFYILTSKELGRGKFAVVRQCISKSTGQEYA
AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS
LCLPELAEMVSENDVIRLIKQILEGVYYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF
GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYLNISQVNV DYSEETFSSVSQ LATDFIQSLLVKNPEKRPTAEICLSH SWLQQWDFEN

FIGURE 1G

LFHPEETSSSSQTQDHSVRSSSEDKTSKSSCNGTCGDREDKENIPEDSSMVSKRFRFDDSL
PNPHELVSDDL

SEQ ID NO: 150_W44160_M DRAK2_M

MSRRRFDCRSVSGLLTTTPQTPIKTENFNFFYTLPKELGRGKFAVVRQCISKSTGQEYA
AKSLKKRRRGQDCRAEILHEIAVLELARSCPHVINLHEVYENATEIILVLEYAAGGEIFN
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNNIVHLDLKPQNILLSSIIYPLGDIKIVDF
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYNISQVNVVDYSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENIPEDGSLVSKRFRFDDSL
PSPHELVPDLFC

SEQ ID NO: 151_H01248_H, DRAK1_H

MIPLEKPGSGGSSPGATSGSGRAGRLSGPCRPPPPQARGLLTEIRAVVRTEPFQDGYS
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEI IHEIAVLELAQDNPW
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR
DVVHLDLKPQNILLTSESPLGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI
SMATDMWSIGVLTYVMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSESAVDFIRT
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDTDKSE
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAISKRFKFEEPLLQEIPGEFIY

SEQ ID NO: 152_AA021445_H

MPARIGYYEIDRTIGKGNFAVVKRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF
CHCRNIVHRDLKAENLLLDANLNKIIADFGFSNLFPTGQLLKTWCGSPPYAAPELFEGKE
YDGPKVDIWSLGVVLYVLVCGALPFDGSTLQNLRARVLSGKFRI PFFMSTECEHLIRHML
VLDPNKRLSMEQICKHKWMKLGADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL
DKEQTLQSLRSDAYDHYSAIYSLLCDRHKRHKTURLGALPSMPRALAFQAPVNIQAEQAG
TAMNISVPQVQLINPENQIVEPDGTLNLDSEGEEPSPEALVRYLSMRRTVGVADPRTE
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNLLPMQNLQPTGQLEYKEQSLLQPPTLQ
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPDQ
EAVQRYLANRSKRHTLAMTNPTAEI PPDLQRQLGQQPFRSRVWPPHLVPDQHRSTYKDSN
TLHLPTERFSPVRRFSDGAASIQAFAKHALEKMGNSSIKQLQQECEQLQKMYGGQIDERT
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQPSPLQAACENQPALLTHQLQRLRIQPS
SPPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQPENCSSPPN
VALTCLGMQQAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMOMQHRTNL
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYPDQAHLPHPLFSDQSRGSPSSYSPST
GVGFSPTQALKVPPLDQFPTFPFSAHQPPHYTTSAQQALLSPTPPDYTRHQQVPHILO
GLLSPRHSLTGHSDIRLPPTFAQLIKRQQQQRQQQQQQQQQEQEYQELFRHMNOGDAGSL
APSLGGQSMTERQALSQNADSYHHHTSPQHLLQIRAEQCVSQASSPTPPHGYAHQPALM
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG
IHPYGHQPTAAFSKNKVPSPREPVI GNCMDRSSPGQAVELPDHNGLGYPARPSVHEHHRPR
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE
CGASLGGHEHPDLSDGSQLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153_2R22-5-11_H

MTAVYMNGGGLVNPHYARWDRRDSVESGCQTESSKEGEEGQPRQLTPFEKLTQDMSQDEK
VVREITLGRIGFYRIRGEIGSGNFSQVKLGIHSLTKEKVAIKILDKTKLDQKTQRLLSR
EISSMEKLHHPNIIIRLYEVVETLSKLHLVMEYAGGGELFGKISTEGKLSEPESKLI FSQI
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

7/113

FIGURE 1H

LFRDEHYIGIYVDI WALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR
LIRGVLQQIPTERYGIDCIMNDEWMQGVYPPTPLEPFQLDPKHLSETSTLKEEENEVKST
LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPMMLPDPKERDLKKGS
RVYRGIRHTSKFCSIL

SEQ ID NO: 154_R31237_1_H, AAC33487

MSTRTPLTPTVNERDTENHTSHGDGRQEVTSTRTSRSGARCRNSIASCADQPHIGNYRLLK
TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPSTSLQKLFREVRIMKILNHPNIVKLFE
VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK
AENLLLDADMNIKIADFGFSNEFTVGGKLDFTFCGSPPYAAPELFQGGKYDGPVDVWSLG
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRGTTLEQ
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT
YLLLGRKSSSELDASDSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQRSVSSSQKQRRYS
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPMLGNASNPKN
ADIPERKKSSTVPSSNTASGGMTRNTYVCSERTTADRHSVIQNGKENSTIPDQRTPVAS
THSISSAATPDRI RFPRTASRSTFHGQPRERRTATYNGPPASPSLSHEATPLSQTRSRG
STNLFSLKLSKLTRSRNVSAEQDENKEAKPRSLRFTWSMKTTSMDPGDMMREIRKVL
ANNCDYEQRRERFLFCVHGDGHAENLVQWEMEVCCKLPRLSLNGVRFKRISGTSIAFKNIA
SKIANELKL

SEQ ID NO: 155_W90839_M

KGPSWSSRSLGARCRNSIASCPEEQPHVGNRYRLLRTIGKGNFAKVKLARHILTGREVAIK
IIDKTQLNPSSSLQKLFREVRIMKGLNHPNIVKLFEVVIETEKTLYLIMEYASAGEVFDYLV
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLDAAENIKIADFGFSNEFTL
GSKLDFTFCGSPPYAAPELFQGGKYDGPVDIWSLGVILYTLVSGSLPFDGHNKELRERV
LRGKYRVPFYMSTDCESILRRFLVLNPAKRCCTLEQIMKDKWINIGYEGEELKPDTELKEE
RMPGRKASCSAVGSGSRGLPPSSPMVSSAHNPNAEIPERRKDSTSTPNLPPSMMTRRN
TYVCTERPGSERPSLLPNGKENSSGTSRVPPASPSHSLAPPSGERSRLARGSTIRSTFH
GGQVRDRRAGSGSGGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLTSKLTRRVTD
PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156_406786.5_H

MEVGGLTVFEEDQRCLSQSLPLPVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSRLCQS
RTALSEDRWSSYCLSSLAQNICSTKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS
PLLPAVPCNPNAKIFTVDAKTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSDSDVVE
ALSEEHMEADGHAADVFGTVVDIIITRSGEKIPVSVWMKMRQERRLCCVVVLEPVERVST
WVAFQSDGTITSCDSLFAHLHGYVSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIORSV
GRARDGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI
NHSFALTFLFGYGKTELLGKNITFLIPGFYSYMDLAYNSSQLPDLASCLDVGNESGGER
TLDPWQGGQDPAEGGQDPRINVVLGGHVPRDEIRKLMESQDIFTGTQTELIAGGQLLSC
LSPQPAPGVDNVPEGSLPVHGEQALPKDQQITAGREEPVAIESPGQDLLGESRSEPVDV
KPFASCEDSEAPVPAEDGGSDAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ
LAGGSLLMHCPCYGSEWGLWWRSDQLAPSPSGMAGLSFGTPTLDEPWLGVENDEELQTC
LIKEQLSQLSLAGALDVPHAEVLPTECQAVTAPVSSCDLGGRDLCGGCTGSSSACYALAT
DLPGGLEAVEAQEVDVNSFSWNLKELFFSDQTDQTSNNCSCATSELRETPSSLA VGSDPD
VGSLOEQGSCVLDRELLLLTGTCVDLGGRRFRESVGHDPTEPLEVCLVSSEHYAASD
RESPGHVPSTLDAGPEDTCPSAEPRNVQVTSTPVI VMRGAAGLQREIQEGAYSGSCYH
RDGLRLSIQFEVRRVELQGPTPLFCCWLKDLLHSQRDSAARTRFLASLPGSTHSTAAE
LTGPSLVEVLRARPWFEEPPKA VELEGLAACEGEYSQKYSTMSPLGSGAFGFVWTAVDKG
KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLEIAILSRVEHANI I KVLDFENQGFFQLV

FIGURE 11

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDI IHRDIK DEN
IVIAEDFTIKLIDFGSAAYLERGKLFYTFCTIEYCAPEVLMGNPYRGPELEMWSLGVTL
YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVDPWVTQ
PVNLADYTWEVFRVKNKPESGVLSAASLEMGNRSLSDVAQAQELCGGPVPGEAPNGQGCL
HPGDPRLT

SEQ ID NO: 157_AA544838_M 406786_M

TRPHPCLEPLASFI FRQLVSAVGYLHSQGI IHRDIK DENIVIAEDFTIKLIDFGSAAYL
ERGKLFYTFCTIEYCAPEVLIGNPYRGPELEMWSLGVTLYTLIFEENPFCEVEETMEAV
IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLIRDPWVTQPVNLASYTWEVCRTNQPS
GLLSAASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDP SLPV

SEQ ID NO: 158_AA785735_H

MVMADGPRHLQRGPVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKI IDKSQLDVN
LEKIYREVQIMKMLDHPHI IKLYQVMETKSMYLVTEYAKNGE IFDYLANHGRLNESEAR
RKFWQILSAVDYCHGRKIVHRDLKAENLLDNMNIKIADFGFGNFFKSGELLATWCGSP
PYAAPEVFEGQQYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRI PYFM
SEDCEHLIRMLVLDP SKRLTIAQIKEHKWMLIEVPVQRPVLYPQE QENEPSIGEFNEQV
LRLMHS LGIDQQKXIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
AEQTVAKAQTVGLPVTMHS PNMRLLSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT
PKVNGCLLDPVPPVLVRKGCQSLPSNMSETS IDEGLETEGEAEEDPAHAFAEFQSTRSGQ
RRHTLSEVTNQLVVM PGAGKIFSMNDSPLDSVDSEYDMG SVQRD LNFL EDNPSLKDIML
ANQPSPRMTSPFISLRPTNPAMQALSSQKREVHNRS PVSFREGRRASDTSLTQGI VAFRQ
HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
LPASVHPQLSPRQSLETQYLQHLRQKPSLLSKA QNTCQLYCKEPPRSLEQQQLQEHRLQOK
RLFLQKQSQLQAYFNQM QIAESSYPQPSQQLPLPRQETPPPSQQAPPFSLTQPLSPVLEP
SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPA
PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLAL
SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159_AA207220_H

MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRRHYEFLETG
KGTYGKVKKARESSGRLVAIKSIRKDKI KDEQDLMHIRREIEIMSSLNHPHIIAIEHVFE
NSSKIVIM EYASRGDLYDYISERQQLS EREARHFFRQIVSAVHYCHQNRVVRDLKLEN
ILLDANGNIKIADFGLSNLYHQGKFLQTF CGSPLYASPEIVNGKPYTGPEVDSWSLGVL
YILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS
HWWVNWGYATR VGEQEAPHEGGHPGSDSARASMA DWLRRSSRPLENGAKVCSFFKQHAP
GGGSTTPGLERQHSLKKS RKENDMAQSLHSDTADDTAHRPGKSNLKL PKGILKKKVSASA
EGVQEDPPELSPI PASPGQAAPLLPKKGILKKPRQRESGYYSPEPSES GELL DAGDV FV
SGDPKEQKPPQASGLLLHRKGILKLNKFSQTALELAAPTTFGSLDELAPPRPLARASRP
SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDP
LGDS CFSLTDCQEV TATYRQALRVCSKLT

SEQ ID NO: 160_AA426580_H, MAK_V_H

MPAAAGDGLLGEPAA PGGGGAEDAARPAACEGSFLPAWVSGVPRERLRDFQH HKRVGN
YLIGSRKLGE GSF AKVREGLH VLTGEKVAI KVIDKKRAK KDTYVTKNLRREGQIQQMIRH
PNITQLLDILETENSYYLVMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA
GVVHRDLKIENLLLDENNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY
GPKIDVWSIGVNMYAMLTGTLPTVEPFSRLALYQKMVDKEMNPLPTQLSTGAISFLRSL
LEPDPVKRPNIQQALANRWLNENYTGKVP CNVTYPNRISLEDLSPSVVLHMTEKLG YKNS

FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCKYKTRLYQIEKYRAPKESYEA
SLDTWTRDLEFHAVQDKPKKEQEKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA
LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNVCVASSSMEFIPVPPPTPRIVKKPEPHQP
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS
PGLPSGSMSPHLHTPLHPTLVSFHEDKNSPPKEEGLCCPPPVPSNGPMQPLGSPNCVKSR
GRFPMMGIGQMLRKRHQSLQPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161_Z36720_H

MDTKLNLMLNEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI
DTQAGWPEVLELVRAMQQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG
RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQKDKGELSAEQGIWATLMTLV
IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAEERLPPIRASGLG
ADPAQAVVSPGQGDGVPGPAQAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAPGRVNV
VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTPGPGPQCPGPPGLPAQARATHSGGETPP
RAALLKGAVAPGFSRRDLVFPSIFCACLGISIHIQEMDTPGEMLMTGRGSLGPTLTTEAP
AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEEQRAGAEPG
TRPSLARSDDNDHEVGALGLQOGKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEAGSV
VLDDSPAPPAPFEHRVSVKETSISAGYEVCOHEVLGGGRFGQVHRCTEKSTGLPLAAKI
IKVKSADREDVKNEINIMNQLSHVNLIQLYDAFESKHSCTLVMEYVDGGELFDRITDEK
YHLTEL DVVLFTTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKI IDFG LARRYKP
REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVI TYMLLSGLSPFLGETDAETMNFIV
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCMSATQCLKHEWLNNLPAKASRSKTRLK
SQLLLQKYIAQRKWKKHFYVVTAAANRLRKFTSP

SEQ ID NO: 162_SGK088_H

GEMALFECLVAGPTDVEVDWLCRGRLLQPALLKCKMHFDGRKCKLLLT SVHEDDSGVYTC
KLSTAKDELTC SARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFG
CPMEES ENLRLRQDGG LHS L HIAHV GSEDEGLYAVSAVNTHGQAHC SAQLYVEEPRTAAS
GPSSKLEKMPSIPEEPEQGELERLSIPDFLRPLQDLEVGLAKEAMLECQVTGLPYPTISW
FHNHGHRIQSSDDRMTQYRDVHRLVFPVAVGPQHAGVYKSVIANKLGAACYAHLYVTDVV
PGPPDGAPQVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQHQVVGSDQWTALVTGLRE
PGWAATGLRKGVQHIFRVLSTTVKSSSKPSPSEPVQLLEHGPTLEEAPAMLDKPDIVYV
VEGQPASVTVTFNHVEAQVVWRSCRGALLEARAGVYELS QPDDDQYCLRICRVSRDMGA
LTCTARNRHGTQTCSVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD
EVLLTSSHVSFVYEENECSLVVLSTGAQDGGVYTCTAQN LAGEVSCKAELAVHSAQTAM
EVEGVGEDEDHGRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFIPSQAKPKAS
ARREARLLARLQHDCVLYFHEAFERRRGLVIVTELCTEELLER IARKPTVCESEIRAYMR
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRI CDFGNAQELTPGEPQYCYGTP
EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFVGENDR TLMNIRNYNVAFEETTF
LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKFLSRRRWQRSQ
ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEELEELPSVPRPLQP
EFGSGRVSLTDIPTEDALGTPETGAATPMDWQEQGRAPSQDQEA PSPEALPSPGQEPAA
GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGP GATRLARGGLGEG
EYAQRLQALRQRLLRGGPEDGKVSGLRGPLESLGGRARDPRMARAASSEAPHHQPPLE
NRGLQKSSSFSQGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPSSPARP
SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVRASKPAPPPQALQTLALP
LTPYAQIIQSLQLSGHAQGPSQGPAAAPPSEP KPHAAVFARVASPPPGAPEKRVPSAGGPP
VLAEKARVPTVPPRPGSSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG
PFRGAEEEDGIYRPSAGTPELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRT P
PAQRHPAWEARGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQ RSGSSSEDSSGGAS

10/113

FIGURE 1K

GRSTPLFGRLRRATSEGESLRRRLGLPHNQLAAQAGATTTPSAESLGSEASATSGSSAPGES
RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPVFHIIKLKDQVLLEGEAA
TLLCLPAACPAPHISWMKDKKSLRSEPSVIIVSCDKGRQLLSIPRAGKRHAGLYECSATN
VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW
HPVSSGIPDCYYNVTHLPVGVTVRFRVACANRAGQGPFSSNSSEKVFVRGTQDSSAVPSAA
HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSSLKAVGPP
PQTTPRRHRGLQAARPAEPTLPSTHVTPEPKPFVLDGTPIIPASTPQGVKPVSSSTPVY
VVTSFVSAPPAPPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP
PQKPYTFLEEKARGRFGVVRACRENATGRTFVAKIVPYAAEGKPRVLQOEYEVLRTLHHER
IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFYSEDDVATYMVQLLQGLDYLHGHV
LHLDIKPDNLLLAPDNALKIVDFGSAQYPNPQALRPLGHRTGTLEFMAPEMVKGEPIGSA
TDIWGAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLSV
HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRRAEAATRHKVLLR
SYPGGP

SEQ ID NO: 163_AA542015_M SGK088_M
ATDIWGAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFADFQLYPNTSQSATLFLRKVLS
VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRRAEAATRHKVLL
RSYPGSP

SEQ ID NO: 164_R19772_H
MKGGDRAVTRGPSLGWLFACCCCFPCRDAYSHSSSENGGKSESVANLQAQPSLNFIHSS
PGPKRSTNTLKKWLTSPVRRNLNSGKADGNIIKKQKVRDGRKSFDLGSPKPGDETTPQGDS
ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLAARQASTEVP TAADLVNA
IEKLVKNKLSLEGSSYRGSCLKDPAGCLNEGMAPPTPPKNPEEEQKAKALGRMFVLNELV
QTEKDYVKDLGIVVEGFMKRIEEKGVPEDMRGDKIVFGNIHQIYDWHKDFFLAELEKCI
QEODRLAQLFIKHERKLHIYVWYCQNKPRSEYIVA EYDAYFEEVKQEINQRLTLSDFLIK
PIQRITKYQLLLKDFLRYSEKAGLECSDEKAVELMCLVPKRCNDMMNLGRLQGFEGTLT
AQGKLLQQDTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGS LTPGYMFKRSIKMN
YLVLEENVNDNDPCKFALMNRETSEVVVLOANADIQQAWVQDINQVLETQRDFLNALQSP
IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPLKISTSNNGSP
GFEYHQPGDKFEASKNDLGCGNGTSSMAVIKDYYALKENEICVSQGEVVQVLAVNQNMCMC
LVYQPASDHSPAAEGWVPGSILAPLTKATAAESDGSIIKKSCSWHTLRMRKRAEVENTGK
NEATGPRKPKDILGNKVS VKETNSSESECEDDLDPNTSMEILNPNFIQEVAPFLVPLVD
VTCLLGDTVILQCKVCGRPKPTITWKGPQDQNILDTDNSSATYTVSSCDSGEITLKI CNLM
PQDSGIYTCIATNDHGTTSTSATVKVQGVPAAPNRP I AQERSCTSVILRWLPPSSTGNCT
ISGYTVEYREEGSQIWQQSVASTLD TYLVIEDLSPGCPYQFRVSASNPWGISLPSEPSEF
VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATRKDVAVKFNKMM
KKKEQAAHEAALLQHLQHPQYITLHDTYESPTSYILILELMDDGRLLDYL MNHDELMEEK
VAFYIRDIMEALQYLHNCRVAHLDIKPENLLIDLRI PVPRVKLIDLEDAVQISGHFHIHH
LLGNPEFAAPEVIQGIPVSLGTDIWSIGVLTYYMLSGVSPFLDESKEETCINVC RVDFS
PHEYFCGVSNAA RDFINVILQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI
ERRKHQNDVRPIPNVKSYIVNRVNQGT

SEQ ID NO: 165_5R72_8_2_H
MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLVVEMSQTSSIGSAESLISLERK
KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEEIIYTFGR
ILGKGSFGIVIEATDKETETKWAIIKKVNKEKAGSSAVKLLEREVNIIKSVKHEHIIHLEQ
VFETPKKMYLVMELCEDGELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHRDLK
LENIMVKSSLIDNNEINLNIKVTD FGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

11/113

FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPFFLASSEAKLFELIRKGE LHFENAVWNSISDCAKSVLKQ
LMKVDPAHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEEK NKPS
TEEKLSYQPWGNVPETNYTSDEEEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE
IKGEMEKTPTVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166_SGK309_H

MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN
VALKVESAAQQPKQVLKMEVAVLKKLQSGSLGQDGKEEMMKPGAKRGKDHVCRFIGCGRNE
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIIHVSGLHHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHD
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMKEKEYEHRMMLKHMPSEFHLFLDHIASLDY
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG
GQCDASAWGPAPGEHRGCATGRAPEXPGECTPNSAREALXGAGPQSPPCPPPRGSXGXSL
GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLLSPPIPSLVPLPCSSXAPCPPPI SLLARPLF
PVPSPALASLCLPSSSSSSVSFTLRRPSA

SEQ ID NO: 167_AA234451_H

MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAAQQPKQV
LKMEVAVLKKLQGDHVCRFICGRNDRFNYYVVMQLQGRNLADLRRSQSRGTFTISTTLR
LGRQILESIESIHSVGSXHRDIKPSNFMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP
RAVAGFRGTVRYASINAHNRNEMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE
RYDHRMLMLKHLPPFEFSIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT
GNDGSLTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP
VGVSPDKLPGSLGHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL
GSPIRVRSEITQPDRIPLVRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168_AA435956_H

TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSFQLFMFQLLRGLAYIHHQHVLHRDLKPQN
LLISHLGELKLADFGARAKSIPSQYSSSEVVTWYRPPDALLGATEYSSSELDIWGAGCI
FIEMFQGGQPLFPVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPWFPLPTPRSLHV
VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV
RLKPEMCDLLASYQKGHPAQFSKCW

SEQ ID NO: 169_AA626859_H

NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIKICDFGFAQILIPGD
AYTDYVATRWRAPPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
TLGKLI PRHQSI FKSNGFFHGISIPEPEDMETLEEKFSVDVHPVALNFMKGCLKMNPDDR
LTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQNQLLPLIPGSHISPTPDGRKQVLQ
LKF DHL PNI

SEQ ID NO: 170_AA061797_M

KIALREIRMLKLKHPNLVNLI EVFRRKRKMHLVFEYCDHTLLNELERNPNNGVSDGVIKSV
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMKICDFGFARILIPGDAYTDYVATR
WRAPPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI
PRHQSI FRSNQFFRGISIPEDMETLEEKFSNVQPVALSFMKGCLKMNPDERLTCAQL
LDSAYFESFQEDQMKRKARSEGRSRRRQQNQLLPLIPGSHISPTPDGRKQVVQLKFDH
LPNI

SEQ ID NO: 171_AA397553_H

MPNSERHGGKKGSGGASGTLQPSGGGSSNSRERHRLVSKHKRHKSKHSDMGLVTPEA
ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSDDLHKHRHHQHRRSR

12/113

FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRI SGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH
KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSOSSKQDDSPSGA
SYGQDYDLSPSRSHTSNNYDSYKKSPGSTSRRQSVSPPYKEPSAYQSSTRSPSPYSRRQR
SVSPYSRRRRSSSYERSGSGYSGRSPSPYGRRRSSSPFLSKRSLRSRPLPSRKSMKSRSRSP
AYSRHSSSHSKKKRSSSRSRHSSI SPVRLPLNSSLGAELSRKKKERAAAAAAAKMDGKES
KGSPVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTVKNSSDTGK
VKLDENSEKHLVKDLKAQGTRDSKPIALKEEIVTPKETETSEKETPPPPLPTIASPPPPLP
TTTPPPQTPPLPPLPPI PALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSKTSASVSSQAN
SQPPVQVSVKTQVSVTAAI PHLKTSTLPPPLPPLPPLPGGDDMDSPKETLPSKPVKKEKEQ
RTRHLLTDLPLPPELPGGDLSPDPSPEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG
KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPITAIREIKILRQ
LIHRSVVMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDLMLGLESGLVHFSEDHIKFSM
KQLMEGLECHYCHKNFLHRDIKCSNILLNNSGQIKLADFGGLARLYNSEESRPYTNKVITLW
YRPPPELLLGEERYTPAIDVWSCGCGILGELFTKKPIFQANLELAQLELISRLCGSPCPAVW
PDVIKLPYFNTMKPKKQYRRRLREEFSFI PSAALDLLDHMLTLDPSKRCTAEQTLQSDFL
KDVELSKMAPDLPHWQDCHELWSKKRRRQSQSGVVVEPPPSKTSRKETTSGTSTEPVK
NSSPAPPQPAPGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDL SIPQMAQLLNI
HSNPQMQQLEALNQSI SALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS
STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQGPRRTPTMPQEEAAACPPHIL
PPEKRPPEPPGPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPHHEH
QALRPMEYSTRPRPNRTYGN TDGPETGFS AIDTDERN SGPALTESLVQTLVKNRTFSGSL
SHLGESSYQGTGSVQFPGDQDLRFARVPLALHPVVGQPFLLKAEGSSNSVVAETKLQNY
GELGPGTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVPI

SEQ ID NO: 172_AA789239_H

MEMYETLGKVGESYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE
NLVNLI EVFRQKKKIHLVFEFIDHTVLDELQHYCHGLESKRRLKYL FQILRAIDYLSNN
VI IHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVLKDTSYG
KYVPVDI WALGCMIIEMATGNPYLPSSDLDLLHKIVLKVXFMPPELKAKLLQEAKVNSLI
KPKESKENELRKDERKTVYTNTLLSSSVLGKEIEKEKKPKEIKVRVIKVKGGRGDI SEP
KKKEYEGGLGQQDANENVHPMSPTDKLV TIEPPNPINPSTNCNGLKENPHCGGSVTMPPI
NLTNSNLMAANLSSNLFHPSVRLTERAKKRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI
FNERTGHSDQMANENKRKLNF SRSDRKEFHFPPELPVTIQSKDTKGMEVKQIKMLKRESKK
TESSKIPTLLNVDQNQEKEQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173_AA124976_M

LADIVHACLQIDPAERTSSTDLLRHDYFTRDGFIEKFIPELRAKLLQEAKVNSFIKPKEN
FKENEPVRDEKKS VFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIKAKGGKGDVPDQKKP
EYEGDHRQQGTADDTQPSSLDKKPSVLELTNPLNPSSENSDGVKEDPHAGGCMIMPPINLT
SSNLLAANLSSNLSHPNSRLTERTKKRRTSSQTIGQTLNSNRQEDTGPTQVQTEKGAFNE
RTGQNDQISSGNKRKLNF PKCDRKEFHFPPELPFTVQAKEMKGMEVKQIKVLKRESKKTDS
SKIPTLLSMDPNQEKEQEGGDGDCEGKNLKRNRFFFSR

SEQ ID NO: 174_AA575635_M CCRK_M

SASGQLKIADFGGLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVDLWAVGCIMG
ELLNGSPLFPGENDIEQLCCVLRILGTSPSRVWPEITELPDYNKISFEEQAPVPLEEVLP
DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTAPLPAHPSELPIPQRPGGPAPKAHP
GPPHVHDFHVDRIEESLLNPELIRPFIPEG

FIGURE 1N

SEQ ID NO: 175_AA631990_H

MITSI STEKSGH THYPFMITTLQYYRGRGGKTAVVRHFS AEGPF AFAEMRHSKRTHCPDW
DSRESWG HESYRGSHKRKRSHSSTQENRHCKPHHQF KESDCHYLEARSLNERDYRDRRY
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNHRHCSSHQSR SXEIV
DTLGE GAFGKVVECIDHGM DGMHVAVKIVKNVGRYREARSEIQVLEHLNSTDPNSVFRC
VQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKL
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKN TDIKVVD FGSATYDDEHHSTLVSTRH
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGP I PQHMIQ
KTRKRKYFH HNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLF DLVRRMLEYDPTQ
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176_AA557536_H

MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA
PEHSPSWPSSRLRLSPQEFGDHPNIISLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGGGL
LQDVHVRSIFYQLLRATRFLHSGHVHRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG
PEDQAVTEYVATR WYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT
STLHQLELILETIPPPSEEXRPRQTL DALLPPDTSPEALDLLRRLLVFAPDKRLSATQAL
QHPYVQRFHCP SDEWAREADV RPRAHEGVQLSVPEYRSRVYQMI LECGSSSGTSREKGPE
GVSPSQAHLHKPRADPQLPSRTPVQGP RP RPQSSPGHDP AEHES PRAAKNVPRQNSAPLL
QTALLNGERPPGAKEAPPLTSLSVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV
RVASVQQVPPRLPPEARPGRRMFSTSALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL
EGHHV

SEQ ID NO: 177_N28606_H, MOK_H

MKNYKAIGKIGEGTFSEVMKMQSLRDGNYYACKQMKQRFESIEQVNNLREIQALRRLNPH
PNILMLHEVVFD RKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLT DGFYT
YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKILTKFKQSRAMNFD FP
FKKGGSGIPLLTNLSPQCLSLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR
KAGFPEHPVAPEPLSNSCQISKEGRKQKQSLKQEEDRPKRGPAYVMELPKLKLSGVVRL
SSYSSPTLQSVLGGSTNGRVPVLRPLKCI PASKKTD PQKDLKPAPQQCRLPTIVRKGG R

SEQ ID NO: 178_AB023153_H, ICK_H

MNRYTTIRQLGDGTYGSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKKNLHA
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLPESAIRNIMYQILQGLAFIHKLG
FFHRDLKPENLLCMGP ELVKIADFG LAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP
IDVWAVGCIMAEVYTLRPLFPGASEIDTIFKICQVLGTPKKT DWPEGYQLSSAMNFRWPQ
CVPNNLKT LIPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS
EKPQKGILERAGPPPYIKPVPPAQPPAKPHTRISSRQH QASQPPLHLTPYKA EVSRTDH
PSHLQEDKPSPLFP SLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKDSDDWAD
LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVG TGN SAPTQT SYQRRDTPT
LRSAAKQHYLKH SRYLPGISIRNGILSNPGKEFIPPNPWSSSGLSGKSSGTMSVISKVNS
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQVRHLAPIPD PSPGYSSLKAMRPHPGRPFLDT
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179_AA839940_M

SSNNGGMSAE E EIGPGAEPMRGPSLATRDWRDET VGT TDLQQGIDPGAVSPEPGKD HAAQ
GPGRTEAGRVSSAAEAAI VVLDDSAAPPAPFEHRVVS IKDTLISAGYTVSQHEVLGGGRF
GQVHRCTERSTGLALAAKI IKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT
LIMEYVDGGELFDRITDEKYHLTEL DVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

14/113

FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL
SGLSPFLGETDAETMNFIVNCSWDFDADTFKGLSEEAKDFVSRLLVKEKSCMSATQCLK
HEWLNHLPAKASGSNVRLRSQQLLQKYMAQSKWKKHFHVVA AVNRLRKFP T C P

SEQ ID NO: 180_AA460132_H

MAAARATTPADGEEPAPAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGAAVIK
HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVLDLYVLEKAF LSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 181_SGK034_H

QREKVNQGNMPGLQSTFLAMDTEEGVEVVWNE LHF GDRKAFAAHEEKIQT VFEQLVLVDH
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKT KKNHKAMNARAWKRWCTQILS
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALPDDLRSPIRAEREELR
NLHFFPPEYGEVADGTAVDIFSF G MCALEMAVLEIQ TNGDTRVTEEA IARARHSLSDPNM
REFILCCLARDPARRPSAHSLLFHRVLF EVHSLKLLAAHCFIQHQY LMPENVVEEKTAM
DLHAVLAELPRPRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAP
PPEEVQKAKTPTPEPFDSETRKVIQMOCNLERSEDKARWHLTLLLVL EDR LHRQLTYDLL
PTDSAQDLASELVHYGFLHEDDRMKLA AFLESTFLKYRG TQA

SEQ ID NO: 182_AA103218_M SGK034_M

HASAPEYGEVNDGTGFVDIFSF G MCALEMAVLEIQANGDTRVTEEA IARARHSLSDPNMR
EFILSCLARDPARRPSAHNLLFHRVLF EVHSLKLLAAHCFIQHQY LMPENVVEEKTAM
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAP
PEEAQKAKTPTPEPFDSETRKVVQMOCNLERSEDKARWHLTLLLVL EDR LHRQLTYDLL
TDSAQDLAAELVHYGFLHEDDRTKLA AFLETTFLKYRG TQA

SEQ ID NO: 183_NEK7_H, N34132_H

MSGGAAEKQSSTPGSLFLSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT
MDKDSRGAAATTTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH
REETVTATATSQVAQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPP
ARSGSGGSAKEPQEERSQQQDDIEELET KAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD
TETTVEVAWCELQDRKLT KSERQRFKEEAEM LKGLQHPNIVRFYDSWESTVKGKKCIVLV
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLI IHRDLKCDNIFITGP
TGSVKIGDLGLATLKRASFASVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEY
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLNHAFQ
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESL KQQVEQSSASQ
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQQLQYQQPSISVLS DGTVD SGQG
SSVFTESRVSSQQT VSYGFPXHEQAHSTGTVP GHI PSTVQAQSQPHGVYPPSSVQQGIQQ
TAPPQQT VQYSLSQTSTSS EATTAQPV SQPQAPQVLPQVSAGKQSTQGV SQVAPAEPVAV
AQPPATQPTTLASSVDSAHS DVASGMSDGNENVPSSSGRHEGRTTKRHYRKS VRSRSRHE
KTSRPKLRILNVS NKGDRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNDFILAIE
RESFVDQVREIIEKADEMLSEDVSVEPEGDQGL ES LQ GKDDYGFSGSQKLEGEFKQPIPA
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN
LSHSASSLSLQQAFSELRR AQMTEGPNTAPPNFSHTGPTFPVVPFLSSIAGVPTTAAAT
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSVV
SSITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGPKPPA
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

15/113

FIGURE 1P

HSSTTGLAFSLSAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL
 LPQVPSIPPLVQPVANVPAVQQTLIHSQPQALLPNQPHTHCPEVDSDTQPKAPGIDDIK
 TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP
 TNLPLGTVALPVTVPVTPGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTL
 PSEQLPFPFGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSAVGPVSMAPTAITEAGTQP
 QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESS
 VLSSSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTAN
 KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSD
 PEAFLSRDVEDDGGSGSPHSPHQLSSKSLPSQNLQSLSNSFNSSYMSSDNESDIEDDLK
 LELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVPVPAVIIPPAAPLSGRRRRRPTKSKGS
 KSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQTLLHPPGNIPESGQNQLLQPLKPSPSDN
 LYSFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184_BCON3_H

MSEGESQTVLSSGSDPKVESSSSAPGLTSVSPPVSTTTSAASPEEEEESEDESEILEESP
 CGRWQKRREEVNQRNVPIDISAYLAMDTTEEGVEVVWNEVQFSEKKNYKLQEEKVRAVFDN
 LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKTCKKNHKTMEKAWKRW
 CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHHVKTCTREEQKNL
 HFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNGGESSYVPQEAISSAIQLLEDPLQ
 REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLAAHCIVGHQHMIPENALEEITKNM
 DTSAVLAEIPAGPGREPVTLYSQSPALEDKFLDVRNGIYPLTAFGLPRPQQPQQEEV
 TSPVPPSVKTPTEPEAEVETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRLHSCDL
 MPNENIPELAAELVQLGFISEADQSRLTSLEETLNKFNFARNSTLNSAAVTVSS

SEQ ID NO: 185_AA711829_M

LKQFLKKTCKKNHKTMEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK
 IGSVAPDTINNHHVKTCTREEQKNLHFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNG
 GESSYVPQEAISSAIQLLEDLSLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLA
 AHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVTLYSQSPALEDKFLDVR
 RNGIYPLTAFGLPRPQQPQQEEVTSPVPPSVKTPTEPEAEVETRKVVLMQCNIESVEEG
 VKHHLTLLLKLEDKLNRLHSCDLMPNESIPDLAAELVQLGFISEADQSRLTSLEETLNK
 FNFTRNSTLNTATVTVSS

SEQ ID NO: 186_AA099102_H

MSSCVSSQPSSNRAAPQDELGGRGSSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP
 GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR
 CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKSGYGVVK
 LAYNENDNTYYAMKVLSSKKLIRQAAFRRPPRRGTRPAPGGCIQPRGPIEQVYQEIAIL
 KKLDPNVVVLVEVLDDPNEDHLYMVFELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGI
 EYLHYQKIIHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTAPFMAPESLS
 ETRKIFSGKAKDVWAMGVTLYCFVFGQCPFMDERIMCLHSKIKSQALEFPDQPDIAEDLK
 DLITRMLDKNPESRIIVPEIKLHPVWTRHGAELPSEDENCTLVEVTEEEVENSVKHIPS
 LATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP
 PGHRPAPRGGGGSALVRGSPCVESCWAPAPGSPARMHPLRPEEAMEPE

SEQ ID NO: 187_5R69_17_2_H

MQEIPQEQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR
 QTFNKEIKTMKKFESPNIIRIFGICIDETVTPPQFSIVMEYCELGTRELLDREKDLTLG

16/119

FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGT
REKTDVRVKSTAYLSPQELEDFYQYDVKSEIYSFGIVLWEIATGDI PFQGEEDWLSQW
L

SEQ ID NO: 188_H85811_H

MAPVYEGMASHVQVFSPHTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS
QPATTTVSTSLPVPNPSPYPYEQTIVFPGSTGHIIVTSASSTSVTGQVLGGPHNLMRRSTV
SLLDYQKCGKLRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS
EGDYQLVQHEVLCSMTNTYEVLEFLGRGTFGQVVKCWRGTNEIVAIKILKNHPSYARQG
QIEVSILARLSTESADDYNFVRAYECFQHKNTCLVFEMLEQNLYDFLKQNKFSPLPLKY
IRPVLQQVATALMKLKSGLIHADLKPENIMLVDPSPRQPYRVKVIDFGSASHVSKAVCST
YLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP
AEYLLSAGTKTTRFFNRDTSPPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN
MTTDLGSDMLVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLDDFPHSTH
VKSCFQNMIEICKRRVNMVDTVNQSKTPFITHVAPSTSTNLMTFNNQLTTVHNQPSAASM
AAVAQRSMPLQTGTAIICARPDFFQQAALIVCPPGFQGLQASPSKHAGYSVRMENAVPIVT
QAPGAQPLQIQPGLLAQQAQWPSGTQQIILLPPAWQQLTGVAHTSVQHATVI PETMAGTQQ
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAQAQPLNVGVAHVMRQQPTSTTSSRSKQH
QSSVRNVSTCEVSSSQAISSPQRSKRKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT
RERQRQTIVIPDTPSPVSVITISSDTEDEEEQKHAPTSTVSKQRKNVISCVTVHDSPPYS
DSSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDSLV
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITRQQRPGPHFQQQQPLNLSQAQQHI
TTDRGTGSHRRQAYITPTMAQAPYSFPHNSPSHGTVHPHLAAAAAAHLPTQPHLYTYTA
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQVPVSMGPRVLPSTIHPQSQYPAQF
AHQTYISASPASTVYTGYPPLSPAKVNQYPII

SEQ ID NO: 189_DYRK3_H

MMIDETKCPPCSNVLCNPSEPPPPRRRLNMTAEQFTGDHTQHFLDGGEMKVEQLFQEFGNR
KSNTIQSDGISDSEKCSPTVSQGKSSDCLNTVKSNSSSSKAPKVPLTPEQALKQYKHHLT
AYEKLEIINYPEIYFVGPNACKRHGVIGGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII
GKGSFGQVARVYDHLKLRQYVALKMVRNEKRFHRQAAEEIRILEHLKKQDKTGSMNVIHML
ESFTFRNHVCMAFELLSIDLIELIKKNKFQGFVQLVRKFAQSILQSLDALHKNKIIHCD
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF
RCILAELLTGQPLFPGEDEGDQLACMMELLMGPPPKLLEQSKRAKYFINSKGI PRYCSVT
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKGCDYLFIEFLKRCLHWDPSARLTPAQ
ALRHPWISKSVPRPLTTIDKVSGRVVNPASAFQGLGSKLPPVVGIAANKLKANLMSETNG
SIPLCVLPKLIS

SEQ ID NO: 190_AA589241_M DYRK3_M

TRPELLGMPPQKLLLEQSKRAKYFINSKGLPRYCSVSTQTDGRVVLGGRSRRGKKRGPPG
SKDWATAKGC GDYLFIEFLKRCLQWDPSARLTPAQALRHPWISKSTPKPLTMDKVPGKR
VVNPTNAFQGLGSKLPPVVGIAASKLKANLMSETSGSIPLCVLPKLIS

SEQ ID NO: 191_5R72_16_2_H

MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKEPPEINLVLY
PQGLTGEEVYVKVLDLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQQRLLEAKRKEEQEQREILHEIQ
RRKEEIKEEKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHGGSPDFVGNKGHR
ANSSGRSRRERQYSVCNSEDSPGSCIEILYFNMGSPDQLMVHKGKICGSDEQLGKLVYNAL
ETATGGFVLLYEWVLQWQKKMGPFLLTSQEKEKIDKCKKQIQGTETEFNSLVKLSHPNVVR

17/113

FIGURE 1R

YLAMNLKEQDDSI VVDILVEHISGVSLAAHLSHSGPI PVHQLRRYTAQLLSGLDYLHSNS
VVHKVLSASNVLDVAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD
VWRLGLLLLLSLSQGECEYPTI PSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFIN
PQPKMPLVEQSPEDSGGQDYVETVIPS NRLPSAAFFSETQRQFSRYFIEFEELQLLGKA
FGAVIKVQNKLDGCCYAVKRI PINPASRQFRRIKGEVTLLSRLHHENI VRYYNWIERHE
RPAGPGTPPPDSGPLAKDDRAARGQPASD TDGLDSVEAAAPPPILSSSVIEWSTSGERSAS
ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSESDI IFDNEDENSKSKNQDEDCNEK
NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
EKGMHRDLKPVNIFLSDDDHVKIGDFGLATDHLAFSADSKQDDQTDGLIKSDPSGHLTG
MVG TALYVSPEVQGSTKSAYNQKVDLFS LGI IFFEMSYHPMVTASERI FVLNQLRDPTSP
KFPEDFDDGEHAKQKSVISWLLNHDPKRPTATELLKSELLPPPQMEESSELHEVLHHTLT
NVDGKAYRTMMAQIFSQRISP AIDYTYDSDILKGNFSIRTAKMQQHVCETIIRIFKRHGA
VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE
RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEI IYTIYEI IQEFPALQERNYSIYL
NHTMLLKAILLHCGIPEDKLSQVYI ILYDAVTEKLTRREVEAKFCNLSLSNSLCLRLYKF
IEQKGDLOQLMPTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK
VQQHNGI IFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSI AIDK
ISAAVLNMEESVTISSCDLLVSVSGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETELV DHVLQKLRTKVTDERNG
READSNLAVQNLKGSFSNASGLFEIHGATVVP I VSVLAPEKLSASTRRRYETQVQTRLQT
SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
DEIYNIKVEKKVSVLFLYSYRDDYYRILF

SEQ ID NO: 192_R43524_H, HRI_H

MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP
FAVANQLLLVSLLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLLSSFTCSDEFSSLRHH
NRAITHLMRSAKERVQRDPCEDISRIQKIRSREVALEAQT SRYLNEFEELVILGKGGYGR
VYKVRNKLDGQYYAIKKILIKGATKTVC MKVLREVKVLAGLQHPNIVGYHTAWIEHVHVI
QPRADRAAIELPSLEVLSDQEEDREQCGVKNDSSSSSI IFAEPTPEKEKRFGESDTENQ
NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQPLLRN SHLEESFTSTEE
SSEENVNFLGQTEAQYHMLHLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT
KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN
GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLEL FQPFQTEMERA EVLTGL
RTGQLPESLRKRCPVQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLMKII EQ
EKEIAELKKQLNLLSQDKGVRDDGKDGGVG

SEQ ID NO: 193_17000057519457_H

MAAARATTPADGEEPAPAEALAAARERS SRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKT PQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVLDLYVLEKAFLSTHPNTETVFEAF LKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 194_AA013524_M

LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRRRTVQEARALLRCRRAGIA
APVVFVDYASNCLYMEEIEDSVTVRDYIQSTMETEKT PQCLLDLARMGQVLAGMHDQD
LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFVSGLPEDKGVLDLYVLEKAFLSTHPHTETA
FEAF LKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

FIGURE 1S

SEQ ID NO: 195_17000139801197_H, IRAKM_H
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK
YVDQGKSGTRELLWSWAQKNKTIGDLLQVLQEMGHRRAIHLITNYGAVLSPSEKSYQEGG
FPNILFKETANVTVDNVLIPHENEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY
RVEIQNLTYAVKLFKQEKMKQCKKHWRFLSELEVLLLFHHPNILELAAYFTETEFKFLI
YPYMRNGTLFDRLOQCVGDTAPLPWHIRIGILIGISKAIHYLHNVQPCSVICGSISSANIL
LDDQFQPKLTDFAMAHFRSHLEHQSCINMTSSSSSKHLWYMPPEYIRQGKLSIKTDVYSF
GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRGDLSCLSFDDKKVPPCPRNFSAKLFC
LAGRCAATRALKRPSMDEVLTNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE
DDESQNNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSCE
ESWFPKYIVPSQDLRPYKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196_AA840598_M IRAKM_M
MWKRFLSELEVLLLFRRHPHILELAAYFTETEFKCLVYPYMSNGTLFDRLOQCTNGTTPLSW
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ
SSTINMTGGGRKHLWYMPPEYIRQGRLSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR
DLLMELMEKRGDLSCLSFDRKI PPCPRNFSAKLFSLAGRCVATKAKLRPTMDEVLSLE
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHVSPPKEVLGTDRVTQK
TPFECSQSEVTFGLDRNRGNRGSEADCNPSSSHEECWSPELVAPSQDLSPTVISLGSS
WEVPGHSYSGKPMKRCSSGLFCSEHEQSKQ

SEQ ID NO: 197_AA088547_H
MASAVRGSRPWPRLGLQLQFAALLLGTLS PQVHTLRPENLLLSTLDGSLHALSKQTGDL
KWTLRDDPVIIEGPMYVTEMAFLSDPADGSLYILGTQKQGLMKLPFTIPELVHASPCRSS
DGVFYTGGRKQDAWFVVDPESETQMTLTTEGPSTPRLYIGRTQYTVTMHDP RAPALRWNT
TYRRYSAPPMDGSPGKYMSHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTW HQDGL
RQLPHLT LARDTLHFLALRWGHIRLPASGPRDTATLFTSLDTQLLMTLYVGKDETGFYVS
KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYPSGSVALPSQWLLI
GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK
TPDSYLGLGPQDLLAASLTAVLLGGWILFVMRQVVEKQQETPLAPADFAHISQDAQSLHS
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRA
VAVKRLRLRECFGLVRREVQLLQESDRHPNVRLRYFCTERGPQFHYIALELCRASLQEYVEN
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGNILITGPDSQGLGRVVLSDFGLC
KKLPAGRCFSFSLHSGIPGTEGWMAPELLQLLPDSPTS AVDIFSAGCVFYVLSGGSHPF
GDSLRYQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSR
AKQLQFFQDVS DWLEKESEQEPLVRALEAGGCAVVRDNWHEHIS MPLQTDLRKFRSYKGT
SVRDLLRAVRNKKHHYREL PVEVRQALGQVPDGFVQYFTNRFPRLLLHTHRMRSCASES
LFLPYYPDSEARRPCPGATGR

SEQ ID NO: 198_HGP_6644466
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGG
KSLNDLIEERYKASQDPFPAAIILKVALNMARGLKY LHQEKLLHGDIKSSNVVIKGD FE
TIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEAVEENGVIITDKADIFAFGLTLWEM
MTLSIPHINLSNDDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199_AA449542_M
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKNLNHPNIIGYRAFTEASDGSL
CLAMEYGGGKSLNDLIEERNKDSGSPFPAAVILRVALHMARGLKY LHQEKLLHGDIKSS

13/119

FIGURE 1T

NVVIKGFETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV
AFGLTLWEMMTLCIPHVNLPDDDDVEDATFDESDFDDEAYYAALGTRPSINMELDDSYQK
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200_5R57_10_2_M TESK2_M
LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201_AA232253_H
MSSLGASFVQIKFDDLQFFENC GGSGFSVYRAKWISQDKEVAVKKLLKIEKEAEILSVL
SHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWATDVAKGMY
LHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFPWWAPEVIQS
LPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH
QCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRCIEATLERLKKLERD
LSFKEQELKERERRLKMWEQKLTEQSNTPLLPSFEIGAWTEDDVYCWVQQLVRKGDSSAE
MSVYASLFKENNITGKRLLLLLEEDLKDMGIVSKGHIHFKSAIEKLTHDYINLFHFPPL
IKDSGGEPEENEKIVNLELVFGFHLKPGTGPQDCKWKMYMEMDGDEIAITYIKDVTFNT
NLPDAEILKMTKPPFVMEKWIIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ
DEVKAVQLAIQTLFTNSDGNPGSRSDSSADCQWLDTLRMRQIASNTSLQRSQSNPILGSP
FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSSPTQYGLTKNFSSLHLNSRDSGFS
SGNTDTSSERGRYSRDRSRNKYGRGSI SLNSSPRGRYSGKSQHSTPSRGRYPGKFYRVSQS
ALNPHQSPDFKRSRDLHQPN TIPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202_AI375137_H
MGNYKS RPTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTEL RNI FGSDEAFSKVNL
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL
LHSGADIQQVGYGGLTALHIATIAGHLEAADVLLQHGANVNIQDAVFFTPLHIAAAYGHE
QVTRLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVPLH
FCSRFGHHDIVKYLLQSDLEVQPHVUNIYGDTPHLHLACYNGKFEVAKEIIQISGTESLTK
ENIFSETAFHSACTYGKSIDLVKFLLDQNVININHQRDGHGTGLHSACYHGHIRLVQFLL
DNGADMNLVACDPSRSSGEKDEQTCMLWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG
GDGSYVSVSPPLGKIKSMTKEKADILLRAGLPSHFHLQLSEIEFHEIIGSGSFGKVYKG
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCV IQFVGACLNDPSQFAIVTQ
YISGGSLSFSLLEHQKRILDLQSKLIIAVDVAKGMEYLHNLTPQPIIHRDLNSHNIILLYEDG
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT
GEIPFAHLKPAAAAADMAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA
LSQSAGQYSSQGLSLEEMKRSLOQYTPIDKYGYVSDPMSSMHFHSRNSSSFEDSS

SEQ ID NO: 203_H97685_H
MESERSPLYRQLIDLGYLSSSHWNCGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRL
VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE
MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEVGTREIKCCIRQIQELIISRLNQA
VANKLISSVDYLRESFVGTLERCLQSLEKSQDVSVHITSNYLKQILNAAHYVEVTFHSGS
SVTRMLWEQIKQIIQRITWVSPPAITLEWK RKVAQEAIESLSASKLAKSICSQFRTRLNS
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHAPRLARLSLESRLQDVLHLRKP KLG
QELGRGQYGVVYLC DNWGGHFP CALKSVPVPDEKHWNDLAL EFHYMRSLPKHERLVLDLHG
SVIDYNYGGGSSIAVLLIMERLHRDLTYGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH
RDIKLNVL LDKQNRAKITDLGFCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

20/119

FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK
RPLLGIVQPMQLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204_W20810_M

DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSLIRETVCDRQSRPPLTELPPGSPET
PGLEKLKELMIHCWGSQSENRPSPQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG
RNLSAREPSQRGTEMDCPRETMVSKMLDRLHLEEPSGVPVPGKCPERQAQDTSVGPATPAR
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHQPNQGDGRHGTPWYPWTPPNPMTGP
PALVFNNCSEVQIGNYNLSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205_AA744236_H

MGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYKRENEDKVNKAACHLKT
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSAEVCAGIYDILLALIFLHDRGHL
THNNVCLSSVFSVEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPFTT
LPECHGHARDAFSFGLTVESLLTILNEQVSADVLSSFQOTLHSTLLNPIPKCRPALCTLL
SHDFFRNDLFLEVVNFLKSLTLKSEEEKTEFFKFLDRVSCLEELIASRLVPLLLNQLVF
AEPVAVKSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLLSH
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSVDKNTSEDSNFSSSKKSEEPDWSE
PEEPENQTVNIQIWPREPCCDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPKVSSQERPLKVPSELG
LGEEFTIQVKKKPKVDPEMDWFADMIPEIKPSAAFLILPELRTEMVPPKDDVSPVMQFSS
KFAAAEITEGEAEGWEEEGELNWNEDNNW

SEQ ID NO: 206_AI052250_H

MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE
VAVFVFDKKLIDKYQKFEKDQIIDSLKRGVQQLTRLRHPRLLTVQHPLEESRDCLAFCTE
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT
PENIILNKSGAWKIMGDFCVSSTNPSEQEPKFPCKEWDPNLPSLCLPNPEYLAPEYILS
VSCETASDMYSLGTVMYAVFNKGKPIFEVKNQDIYKSFSRQLDQLSRLGSSSLTNIPEEV
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTLQFQDNLQKSQFFKGLPKVL
PKLPKRIVIVQRILPCLTSEFVNPDMPVFPVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ
EPIQILLIFLQKMDLLLTCTPPDEIKNSVLPVMYRALEAPSIQIQELCLNIIPTFANLID
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207_AA278842_H

MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEEQTQV
AKAAFKRFKTLRHPNILAYIDGLETEKCLHVVTAVTPLGIYLKARVEAGGLKELEISWG
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNNGGPPRKGIP
LEQYDPPELADSSGRVVREKWSADMWRLGCLIWVFNGLPRAAALRNPGKIPKTLVPHY
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS
LDAFPEDFCRHKVLPLQLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS
TDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFDTNPATIREQTVKSMALLAPKLN
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPF
APSRVAGVLGFAATHNLYSMNDCAQKILPVLCLTVDPEKSVRDQAFKAIRSFLSKLESV
SEDPTQLEEVEKDVHAASSPGMGAAASWAGWAVTGVSSLTSLKIRSHPTTAPTETNIPQ
RPTPEGVPAPAPTVPATPTTSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVL
AQQDDWSTGGQVSRASQVSNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEPPPDGTR
LASEYNWGGPESSDKGDPFATLSARPSTQPRPDSWGEDNWEGLTDSRQVKAELARKKRE
ERRREMEAKRAERKVAKGPMKLGARKLD

21/113

FIGURE 1V

SEQ ID NO: 208_AA599286_H

MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD
PNNYSANYTEIALQQVSMFRRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSW
ADLGPDKYLSKDFQCLIKLLPSCLPYIYRVTFATANESSALLIRMFNEKGTLDKLIYK
AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLLHASNVMLDGD
CRLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP
PAPSMVAVVLESTLSCEACKNGMPTISRLLQMPPLFSDVLLTTSEKPQFKIPTKLKEALR
IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEERKKRKILARKKSKRSALENSEEHSA
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEAPAQLS
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRSAEASCLHLEGKVLFFYSYSPLPPN
YPLPGKVIAEPVQPQTVLFCRCSCCKQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209_AA425725_H

MSASTGGGGDSGGSGSSSSSQASCGPESSGSELALATPVPQMLQGLLGSDDEEQEDPKD
YCKGGYHPVKIGDVFNTRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVKSAAGHYTETA
VDEIKLLKCVRDSDPSDPKRETIVQLIDDFRISGVNGVHVCMLVLEVLGHQLLKWI I KSNY
QGLPVPCKVSIVRQVLHGLDYLHTKCKI IHTDIKPENILLCVGDAYIRRLAAEATEWQQA
GAPPPSRISIVSTAPQEVLTGKLSKNKRKKMRKRKQKRLLEERLRDLQRLEAMEAATQA
EDSGLRLDGGSGSTSSSGFSGSLFSPASCSILSGSSNQRETGGLLSPSTPFGASNLLVNP
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGGPADIWSTACMAF
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDIPPAFALSGRYSREFFNRRGELRHIHN
LKHGWGLYEVLMKEYEWPLEQATQFSAFLPLPMEYIPEKRASAADCLQHPWLN

SEQ ID NO: 210_SGK022_H

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ
IVRTLDDHKNIIQVYEMLESADGKICLVMELEAGGDVFDVLCVNGGGLPESRAKALFRQMV
AIRYCHGCGVAHRDLKCENALLQGFLNKLTDGFGAKVLPKSHRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLVYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLSISADCQD
LLKRLLEPDMILRPSIEEVSHPWLAST

SEQ ID NO: 211_AA060026_M SGK022_M

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ
IVRTLDDHKNIIQVYEMLESADGKIYLVMELEAGGDVFDVLCVNGGGLPESRAKALFRQMV
AIRYCHGCGVAHRDLKCENALLQGFLNKLTDGFGAKVLPKSRRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLVYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLGISTECQD
LLKRLLEPDMILRPSIEEVSHPWLAST

SEQ ID NO: 212_AA399669_H

MGKGDVLEAAPTTTAYHSLMDEYGYEVGKAIGHGSYGSVYEAFFYTKQKVMVAVKII SKKK
ASDDYLNKFLPREIQQVMKVL RHKYLINFYRAIESTSRVYIILELAQGGDVLEWQRYGA
CSEPLAGKWFSQTLTGIAYLHKSISVHRDLKLENLLDKWENVKISDFGFAKMPVSNQPV
GCSXPYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLFP
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213_AA758539_H

MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE
MDILATVNHGSIKTYEIFETSDGRIYIIMELGVQGDLLFIKCGALHEDVARKMFRLQ
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

24/113

FIGURE 1W

YAAPEVLQSIPIYQPKVYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQKEHRVDFPRSKN
LTCECKDLIYRMLQPDVSQRLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHSAGAEVGKAST

SEQ ID NO: 214_AA883975_H

MSGDKLLSELGYKLGRITIGESYSKVKVATSKKYGTVAIKVVDRRRAPPDFVNKFLPRE
LSILRGVRPHPHIVHVFIEVCNGKLYIVMEAAATDLLQAVQNRGRIPGVQARDLFAQIA
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRAHGYPDLSTTYCGSAAAYASP
EVLLGIPYDPKKYDVWSMGVVLVYVMVTGCMPPDDSDIAGLPRRQKRGVLYPEGLELSERC
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215_AA905446_H

VGRQETGVRRWAFLICQPISPPLTSSEFIQRFLPRELQIVRTL DHKNI IQVYEMLESADG
KICLVMELAEAGGDVFDVNLGGPLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALL
QGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGI PXKMLWQQQKGVSPFTHL
SISADCQDLLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 216_H29974_H

YSLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAE EPCYLWFMFCEGG
DLNQYVLSRRPD PATNKSFMLQLTSAIAFLHKNHIVHRDLKPDN ILITERSGTPILKVAD
FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYMAPEVWEGHYTAKADIFALG
IIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG
IKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 217_AA498104_M H29974_M

PLLLPPPPAAMETGKENGARRGTKSPERKRRSPVQRVLC EKL RPAAQAMDPAGAEVPGEA
FLARRRPDGGGGDV PARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE
LALAEFWALTSLKRRHQNVQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL
GYAE EPCYLWFMFCEGGDLNQYVLSRRPD PATNKSFMLQLTSAIAFLHKNHIVHRDLK
PDN ILITERSGTPILKVAD FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYM
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLE
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 218_AA215311_H

MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI
KSQHPNVIHLEECILQKDMVQKMSHGSSSLYLQLVETSLKGEIAFDPRSAYYLWFMVD
FCDGGDMNEYLLSRKPNRKTNTSFMLQLSSALAFHKNQIIHRDLKPDN ILISQTRLDT
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTD FYMAPEVWEGHYTAKADI
FALGIIIWAMLERITFIDTETKKELLGSYVKQGT EIVPVGEALLENPKMELLPVKKKSM
NGRMKQLIKEMLAANPQDRPD AFELELRVLQIAFKDSSWET

SEQ ID NO: 219_AA018361_H

MRAAFPAGGAGGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPRLDGFILT
ERLGS GTYATVYKAYAKD TREVVAIKVAKKSLNKASVENLLTEIEILKGIRPHIVQL
KDFQWSDNIYLIMEFCAGGDL SRFIHTRILPEKVARVFMQQLASALQFLHERNISHLD
LKPQNILLSSLEKPHLKLADFGFAQHMS PWDEKHVLRGSPLYMAPEMVCQRQYDARVDLW
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALSLYCKALDFFVPA

23/113

FIGURE 1X

LHYEVDAQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARDKPRLL
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSRAGGGSCFTLRFRTSWPELN
T

SEQ ID NO: 220_AA311714_H

MENFILYEEIGRGSKTVVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNI
VTFHEWYETSNHLWLVLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL
KFSNFCLAKVEGENLEEFFALVAAEEGGGDNGENVLKKSMSRVKGSVPYTAPEVVRGAD
FSISSDLWSLGLLYEMFSGKPPFFSESVSELTEKILCEDPLPPIPKDSSRPKASSDFIN
LLDGLLQORDPQKRLTWTRLLQHSFWKKAFAAGADQESSVEDLSLSRNTMECSGPQDSKELL
QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPTPRTSTAVEV
SPGEDMTHCSPQKTSPLTKITSGHLSQQDLESQMRELIYTDSDLVVTPIIDNPKIMKQPP
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV
AGHQEVATRLLHSPFLQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS
SIGIGILNCLVQHSTPVPVPRQCLVYV

SEQ ID NO: 221_SGK384_H

SLAHVLRARQILTEPEVRDYLRLGLVSGRLRYLHQRCILHR

SEQ ID NO: 222_AA210451_M SGK384_M

MGQQHGTRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPGRSTADSRRCPPGYFR
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH
GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNLSKYQDVNTWQHRLQL
AMEYVSIINYLHHSPLGTRVMCDSDNLPKTLQYLLTSNFSIVANDLDALPLVDHDSGV
LICKGHRELHGFVAPEQLWPYGEDTPFQDDLMPQSYNEKVDIWKIPDVSSFLLGHVEGSDM
VRFHLDIHKACKSQIPAERPTAQNVLDAYQRFVHSLRDTVMSQTKEML

SEQ ID NO: 223_SGK071_2_H

EVVAVQMMVECMDDHYASQALEELMPLLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALLEYLHHLDIHRNLKPSNIIILISSDH
CKLQDLSSNVLMTDKAKWNI RAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC
SFMGDTEAMHLRKSRLRQSPGSLKAVLKTMEEEKQIPDVETFRNLLPLMLQIDPSDRITIKD
VVHITFLRGSFKSSCVSLTLHRQMVPASITDMLLEGNVASILGDAGDTKGERALKLLSMA
LASYCLVPEGSLFMPLALLMHMDQWLSCDQDRVPGKRDFASLGKLGKLLGPPIPKGLPWPP
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH
PEEEPLLVMVYSLLAITTTQESSELSSEELQNAGLLEHILEHLNSSLESRDVCASGLGLLW
ALLLDDPILALQRPRKKRAPNHGKPGKPNPASTQSIIVNKAPLEKVPDLISQVLATYPA
DGEMAEASCGVFWLLSLLGCIKEQQFEQVALLLQSIIRLCQDRALLVNNAYRGLASLVKV
SELAAFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGMLLVHLASYEEILPELVSSSM
KALLQEIKERFTSSLVSDSSAFSKPGLPPGGSPQLGCTTSGGLE

SEQ ID NO: 224_AA118352_M SGK071_M

EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL
KPILKTMEEEKQIPGTDVYYLLLPFMLHINPSDLAIKDVMQVTFMSNSFKSSSVALNMQR
QKVPIFITDVLLEGNMANILGSWLCASFVNDNRHCDSGIGSQRLGFDQSVSWTEHPLKD
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEVISIIKQHGRILDILLSTCSLL
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAISSQGQISEEL
EEEGLFQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVVLLLSIQLCPGRVLLVNNAFRGLASLAK

24/113

FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225_018653.9_H

GRGRGAGHARGLRGPAGRRAEPPRSLSRPGPGPGSRAGPAGRGEGSDAAPAGGSGRGFL
RLLPAGLRPQALRSRGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG
GPGPGAGRPERRRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA
ALRNVSGAQYMGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEDI PDTLTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLD SI VNATGE
LAWGVDETLAQLEKVLHLRYSGQYLQNSTASSSTEYQCI PDSTIPQEDYRCWPSYHHGSC
LLSVFNLAEAVDVCESHAQCRAFVVTNQT TWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226_AA396601_M

TRPGCAALRNVSGAQYVGSYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGARRG
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEGI PDTLTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLD SI
VNATGELAWGVDETLAQLETALHLFRSGQYLQNSTSSRAEYQRI PDSAITQEDYRCWPSY
HHGGCLLSVFNLAEAIDVCESHAQCRAFVVTNQT TWTGRKL VFFKTGWNQVVPDAGKTTY
VKAPG

SEQ ID NO: 227_VRK3_H

MISFCPDCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP
KKVKWSSTVTSPLSLFSDGDSSESED TLSSSERSKSGSGSRPPTPKSSPQKTRKSPQVTR
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLKSFQTRDNQGIL
YEAAPTSTLTCDSGPQKQKFSCLKDAKDGRLFNEQNFFQRAAKPLQVNKWKLYSTPLLA
IPTCMGFGVHQDKYRFLVLP SLGRSLQSALDVSPKHVLSERSVLQVACRLDDALEFLHEN
EYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFISMD
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP CGH
WIRPSETLQKYLKVMALTYEEKPPYAMLRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228_S71575_M VRK3_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSALDDNPKHVVSERCVLQVACRLDDALEYLHEN
EYVHGNLTAENVFVN PEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFISMD
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTTEKITRQKQKYLDSPERLVGLCGR
WNKASETLREYLKVMALNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMVP

SEQ ID NO: 229_AA45427_H

MGHALCVCSRGTVI IDNKRYLFIQKLGE GGSYVDLVEGLHDGHFYALKRILCHEQQDRE
EAQREADMHRLFNHPN IRLVAYCLRERGAKEAWLLLPFFKRGTLWNEIERLKDKGNFL
TEDQILWLLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLMDLGSMNQACIHVEGS
RQALTLQDWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGCVLYAMMFEGEPYDMVFQ
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRPHI PLLLSQLEALQPPAPGQ
HTTQI

SEQ ID NO: 230_H05721_H

MAVRQALGRGLQLGRALLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEP RRVG
LGLPNRLRFFRQSVAGLAARLQRQFVVRWGCAGPCGRAVFLAFGLGLGLIEEKQAESRR

25/113

FIGURE 1Z

AVSACQEIQAIF TQKSKPGPDPLDTRRLQGRLEEYLIGQSIGKGCSAAVYEATMPTLPQ
NLEVTKSTGLLPGRGPGTSAPGEGQERAPGAPAFPLAIKMMWNI SAGSSSEAILNTMSQE
LVPASRVALAGEYGAVTYRKS KRGPKQLAPHPNI IRVLRAFTSSVPLLP GALVDYPDVLP
SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTPSRPLAAMMLLQ LLEGVDHLVQQGIAH
RDLKSDNII LVELDPDGC PWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST
ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGYQGKAHLESRSYQEAQLPALPESVPP
DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQQAATLL
ANRLTEKCCVETKMKMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231_AI086865_H

MEKYERIRVVGRGAFGIVHLCLRKADQKLVI IKQIPVEQMTKEERQAAQNECQVLKLLNH
PNVIEYYENFLEDKALMIAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALHHVH
THLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSTPCYISPELCEGKPYNQKSDIW
ALGCVLYELASLKRAFEANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP
PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQGIIMTFGSGSNGCLGHGS
LTDISOPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPLLSIDLGTAHSAAVTGEEDL
GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPPDKCCWRHKQCTGHI IYPFASDCV
RHS LHLHSVNHNCNSRLKDSSSEDSSSSRGAGPTCSHVIESPCFELTPEEEHVERFRYGW
CKSYRPVSVAVIHHPLYHECGADDLNKKRKRKRKRKRKPPIPTQVGPATASPD LGTSMAT
GTPDSTAPITIWRSSEPTGKGQGSKVIKKVKKKKEKEKDKEEMDEKAKLKKKAKKGQLTK
KKSPVKLEPSPPDVSRSL SARQLARMSESSPESREELESEDSYNGRGQGELSSEDI VESS
SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232_AA836348_H

MSVLGEYERHCDSINSDFGSESGGCGDSSPGPSASQGPRAGGAAEQEELHYIPIRVLGR
GAFGEATLYRRTEDDSL VVWKEVDLTRLSEKERRDALNEIIVILALLQHDNI IAYYNHFM
NTLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVSCIHKAGILHRDIKTL
NIFLTKANLIKLG DYGLAKKLNSEYSMAETLVGTPTYMSPELCQGVKYNFKSDI WAVGCV
IFELLTLKRTFDATNPLNLCVKIVQGIRAMEVDSSQYSLELIQMVHSCLDQDPEQRPTAD
ELLDRPLLRKRRRSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG
NTHFAVVTVKEKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLQGAIRQVSCGDDF
TVCVTDEGQLYAFGSDY YGCMGVDKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVLTR
NKEVYSWGCGEYGRGLDSEEDYYTPQKVDVPKALII VAVQCGCDGTFLLTQSGKVLACG
LNEFNKLGLNQCMSGIINHEAYHEVPYTTSFTLAKQLSFYKIRTIAPGKTHTA AIDERGR
LLTFGCNKCGQLGVGN YKKRLGINLLGGPLGGKQVIRVSCGDEFTIAATDEKVLNSKTIR
SNSGLSIGTVFQSSSPGGGGGGGGGEEEDSQESETPDPSGGFRGTMEADRGMEGLISP
TEAMGNSNGASSCPGWL RKELENAEFI PMPDPSPLSAAFSESEKDTLPYEELQGLKVA
SEAPLEHKPQVEASVTELF AFESQLVTSAESCSNLCWEGNTTDS SCVCVQLSAGGG

SEQ ID NO: 233_R86668_H, MKK6_H

MNLLLSYRDVQDYS AIIELVETLQALPTCDVAEQHNVC FHYTFALNRRNRPGDRAKALSV
LLPLVQLEGSVAPDLYCMGRIYKDMFFSSGFQDAGHREQAYHWYRKA F DVEPSLHSGIN
AAVLLIAAGQH FEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLG AQILANDPTQV
VLA AEQLYKLNAPIWYLVSVMETFLLYQHFRPTPEPPGGPPRAHFWLH FLLQSCQPFKT
ACAQGDQCLVLVLEMNKVLLPAKLEVRGTD PVSTVTL SLLEPETQDI PSSWTFPVASICG
VSASKRDERCCFLYALPPAQDVQLCFPSVGH CQWFCGLIQAWVTNPDSTAPAEAEAGAGE
MLEFDYEYTETGERLV LGKGT YGVYAGRDRHTRVRIAIKEI PERDSRFSQPLHEEIALH
RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWG PLKDNESTISFYTRQILQ
GLGYLHDNHI VHRDIKGDNLINTFSGLLKISDFGTSKRLAGITPCTETFTGT LQYMAPE
IIDQGRGYGKAADIWSLGCTVIEMATGRPPFHELGSQAAMFQVGM YKVHPPMPSSLSA

26/113

FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN
STTQSQTFFPCPQAPSQHPPSPPKRCLSYGGTSQLRVPEEPAAEEPASPEESSGLSLLHQE
SKRRAMLAAVLEQELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ
ELRALQGRRLRAQGLGPALLHRPLFAFPDAVKQILRKRQIRPHWMFVLDSLLSRAVRAALG
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR
EILAGKEREYQALVQRALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM
LLNHSFTLHTLLTYATRDDLITYTRIRGGMVCRIWRILAQRAGSTPVTSGP

SEQ ID NO: 234_PAK6_H

MFGKKKKKIEISGPSNFEHRVHTGFDPPQEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT
PIQLAPMKTIVRGNKPKETSINGLLEDFDNISVTRSNSLRKESPTPDQGASSHGPGHA
EENGFITFSQYSSSEDTTADYTTEKYREKSLYGGDDLDPYRGSHAAKQNGHVMKMKHGEA
YYSEVKPLKSDFARFSADYHSHLDSLSKPSSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA
GTSGCSKESLAYSESEWGPSLDDYDRRPKSSYLNTSPQPTMRQRSRSGSGLQEPMPFPG
ASAFKTHPQGHSYNSYTYPRLSEPTMCIPKVDYDRAQMVLSPLSGSDTYPRGPAKLQPS
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSQYISTASYLSSLSLSSSTYPSPSWGSSS
DQQPSRVSHQFRAALQLVVSFGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM
DLRKQQRRELLFNEVVIMRDYHHDNVDMYSSYLVGDELWVMEFLEGGALTDIVTHTRM
NEEQIATVCLSVLRALSYLHNQGVHRDIKSDSILLTSDGRIKLSDFGFCAQVSKEVPKR
KSLVGTPTYWMAPEVISRLPYGTEVDIWSLIGIMVIEMIDGEPPYFNEPPLQAMRRIRDSL
PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235_SURTK106_H

MNDRNEIQMEAKLQSLTIIAQEIICRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI
LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIEKQYEVIIIVPTLLVTIFLILLGVILWL
FIREQRTQQQRSGPQGIAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQ
VPREQLSEVLEQICSGSCGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIQF
HQYLGKHKNLVQLEGCCTEKLPLYMVLEDVAQGDLLGFLWTCRRDVTMDGLLYDLTEKQ
VYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT
IPLKWLAPERLLLRLPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKR
PSSCTHTMYSIMKSCWRWREADRPSPRELRLRLEAAIKTADDEAVLQVPELVVPELYAAV
AGIRVESLFYNYSML

SEQ ID NO: 236_AA098024_M

LQEKHLFHGDVAARNILIQSDLTTPKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL
LRPASIRGDIWSFGILLYEMVTLGAPPYPEVPPTSILQYLQRRKIMKRPSSCSHAMYNIM
KCCWRWSEDSRPLLVLQQLQRLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF
SVL

SEQ ID NO: 237_SGK2ALPHA_H

MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVLLAKRKSDGAF
YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLVDYVNGGE
LFFHLQORERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGL
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDQDVS
QMYENILHQPLQIPGGRTVAACDLLQSLHLKQDQRQLGSKADFLEIKNHVFFSPINWDDL
YHKRLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE
DDDILDC

27/113

FIGURE 1BB

SEQ ID NO: 238_CCRK_H

MDQYCILGRIGEGAHGIVFKAKHVETGEI IALKKVALRRLEDGFPNQALREIKALQEMED
NQYVVQLKAVFPHGGGFVLAFAEFMLSDLAEVVRHAQRPLAQAQVKSYLQMLLKGVAFCHA
NNIVHRDLKPANLLISASGQLKIADFGRLARVFS PDGSRLYTHQVATRSVGCIMGELLNGS
PLFP GKNDIEQLCYVLRILGTPNPQVWPELTELDPY NKISFKEQVPMPL EEVLPDVSPQA
LDLLGQFLLYPPHQRIAASKALLHQYFFTA PLPAHPSELPIPQRLGGPAPKAHPGPPHIH
DFHVD RPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLP GFTLQGLPMA
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239_TESK2_H

MDRSKRNSIAGFP PRVERLEEFEGGGGGEGNV SQVGRVWPSSYRALISAFSRLTRLD DFT
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLI KRDENGYSAVVA
DFGLAEKIPDVSMGSEKLAVVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEI IARIQAD
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLTFNCCNMDPKLRPSFVEIGKTLEEILSRL
QEEEQERDRKLQPTARGLLEKAPGVKRLSSLD DDKIPHKSPCPRRTIWLSRSQSDIFSRKP
PRTVSVLDPYRPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSKSVISLVFDLDAPGPG
TMPLADWQEPLAPPIRRWRS LPGSPEFLHQEACPFVGREESLSDGPP PRLSSLKYRVKEI
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEERPAGSTPATF
STSGIGLQTQ GKQDG

28/113

FIGURE 2A

SEQ ID NO: 1_X69117_H BARK2_H

ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC
AAGGCGACCCCGGCCGCGCCAGCAAGAGGATCGTCCTGCCGGAGCCCAGTATCCGG
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA
CCTCAGGTGAAGTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC
CGCCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTTCTTCTGT
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA
GTGACATCAACTCTTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC
ATTTTTCAAAAATTTATGGAAAGTGACAAGTTCCTAGATTTTGTGCTAGTGGAAAAACGTT
GAATTAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA
GGATTTCGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA
ATCATGTTGTCTCTTGTGTCAGCACAGGAGACTGTCCTTTCATTGTATGTATGACCTATGCC
TTCCATACCCAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTTGCAC
TACCACCTTTCACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTATGCCACTGAA
ATCATTCTGGGTCTGGAACACGTGCACAATCGGTTTGTGTTGTCTACAGAGATTTGAAGCCA
GCAAATATTCTCTTGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCCTGC
GATTTTTCAAAAAGAAGCCTCATGCGAGTGTTGGCACCCATGGGTACATGGCTCCCGAG
GTGCTGCAGAAGGGGACGGCTATGACAGCAGTGCCGACTGGTTCTCCCTGGGCTGCATG
CTTTTCAAACCTTCTGAGAGGTACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACCTTCAGACACCTTCTCTCCTGAA
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTAC
GGAGGCGGCTCACAGGAAGTAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT
GTCTACTTACAAAAGTACCCACCACCCTTGATTCTCCCGGGGAGAAGTCAATGCTGCT
GATGCCCTTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTCATCTCTGAACGCTGGCAGCAAGAA
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG
AGAGCTAAAAATAAGCAACTTGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT
ATGCACGGGTACATGCTGAAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT
TTTTACCTCTTTCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAAATGCATT
TTGTTTCAGAATAAAAGGAGGGAAACAATTTGTCTTGCAATGTGAGAGTGATCCAGAGTTT
GTGCAGTGGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCGT
GCCCCGAAGTTCCTCAACAAACCTCGGTCAGGTACTGTGGAGCTCCCAAAGCCATCCCTC
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2_AA144574_M BARK2_M

CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA
CGTGAGGATATCGGATCTCGGCCTTGCTGTGATTTCTCCAAAAGAAGCCTCATGCCAG
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA
CGTGACGCTTCCAGATGCCTTCTCCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACGCCGTCAA
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

23/113

FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTTTACCTGTTCCCCAACAGACTGGAGTG
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTACTCAGGATAAAGGGAGGGAAGCAATT
TGTCTTGCAATGTGAGAGTGAACCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC
CTTCAATGAGGCCAGAGACTGCTGCGCCGTGCCCCCAAATTCCTCAACAAACCACGGGC
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTACAGAAATAGCAGCGGCCTCTGAAC
CACAGAGCAGCGGGGCTGAAGGAGGGGCCAGCTCTTCAGCCCAGGAGTGGAACGAAG
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTCTTCTGAGCACTGACGGGGCTGCTCCA
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3_AA826850_H

GAAGAGGATGGGCTCGTCCATGTTCGGCGGCCACCGCGCGGAGGCCGGTGTGTTGACGACAA
GGAGGACGTGAACTTCGACCACTTCCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG
CAAGGTGTGCATTGTGCAGAAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCCGGGAGCTGGAGATCCT
GCAGGAGATCGAGCACGTCTTCTTGGTGAACCTCTGGTACTCCTTCCAGGACGAGGAGGA
CATGTTTCATGGTTCGTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA
CGTGCAGTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGAGATCTTCCAXTCTTT
TGTCAACGGCGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTCCGGTGGGGGTGATGGC
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC
CCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGCTGTGGGACCACCTGAGCGAGAAGAG
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTCTGCACTGCGACCCACCTTTGAGCT
GGAGGAGATGATCCTGGAGTCCAGGCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAACAGAGAAAAGCTGAAGAGGAGCCA
GGACCTCCCGAGGGAGCCTCTCCCCGCCCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCCATTGCCCCCTCGGCCGGGAG
CGGCTAGGCCGGGATGCCCCGTGGTCCCTACCCCTTGAGCTGCTTTGGAGACTCGGCTGCC
AGAGGGAGGGCCATGGGCCGAGGCCTGGCATTACAGTTCCACCCAGCCTGGCTGGCGGT
GCCCCAGTGGCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCTCGTGGGCCCCCGAGACCCGCCTA
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG
GGACAGGAGTCTTTGTCCCTGCTCAGCCCGGAGGCTGTGCACGGCCCTCGTCACAAGGTG
ACCCTTGAGCACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC
ATGGGTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAAGTCTCCAGCA
ATTTCTGTATAGTTTTTACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4_AA960957_H

GTCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG
GAATATGGGCGGGAACCACTCCACAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA
CTTTGACCATTTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT
CGTGCAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG
CATCGAGAGGGATGAGGTTCCGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

32/113

FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTCATGGT
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTAC
AGAGGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA
TGTTACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG
CCCCGGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTCAACAT
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCCACATTTGAGCTTGAAGAGATGAT
TCTAGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA
TGGCACAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA
GCTCTTGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCACACTTG
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCTCTTTGTGC
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAGCCCTGGACTTGGA
GCTGGGAAGCCTGGGTTCTGGTCCCATCTCCATGACTGATTACGTGTGACCTCAGACAA
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTAAACACTTCTGCC
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAACCTT
TGATATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC
ATTCGCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA
GGGCACTTCCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCTT
CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT
CTGGCAGGCCACAGTCCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCCTCATTTAAGAAGACTATCCTTACCTTTT
AGTTTCAGCAGTCCTCACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA
TTCAGATGAGAGTTGGGTGCTGAGCATTGGTTACTCCTGCAGAGTGTAATCAGCACCCCC
ATCCAACCTGGCCCGAAAGCCCAGACCTGCAGCAGAACTCTCCAACCTCTCTATCAGCTTTC
AGGGTTTTCTCTCCTGGGAAGGGTGTAAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG
AAAGTTTATTTTACAGGAGGAAAATGGGTTTACACAAAAAGCAAACCTACATTCTGATCTGCT
CAGGGAGAAGCTTGCCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT
TGGAGTCAGGTTTGTGTTTCAATCCAGCCCTGCTGGCTACTAACTAACTGGGAGACCTT
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCTCATTTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG
GATGACTCATAGAATGGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTC
TTCTTCACTCACCCAGCAGGTCAGTTTTTCTGTGCAAAACAAACCTGTTTAGGATTCTTCC
AAATGTTCTTCTGGGGTCTTTTGATATTTGTTTGTACATCCTGCTGAAGTTCGACTGTG
TTTTTATTTTTTTCATCCAACCTTCCATTTTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTATCTCTTAGATTTCTTAAAGACATTTTAAATGTATGGTTAGGTTTTAT
ATTTTTATTTTTTAAAAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTT
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTTTTGCACACTTTTCTTACTTCATGTCCC
CATCAACAACCGTCCTGCTCCCCACCTCCCCCAGGAAATAAGGGGCTGCTCCTCTCCCT
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGA
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTTCTGTTCAAGT
TGGCATTTCTTGTGTTGGAATAAACTATTTCTTGGACATTCCTTC

FIGURE 2D

SEQ ID NO: 5_TBK1_H

TCCTGAGTCTCGAGGAGGCCGCGGGAGCCCGCGGCGGTGGCGCGGGAGACCCGGCTG
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG
ATGTTCAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTTGTG
CATGTGGGAGTTTATACACTGTTTTAGAAGAACCTTCTAATGCCTATGGACTACCAGAAT
CTGAATTCCTTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCAGTCTTT
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG
AAAAGTGTTGGGGTTTTGACCAGTTTTTTGTCAGAACTAGTGATATACTTCACCGAATGG
TAATTCATGTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTATAGCTATA
ATACTGCTACTATATTTTATGAAGTGGTATATAAACAACCAAAATTTATTTCTTCAAATC
AAGAACTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT
TCCCTAAAACCTACTGAGGAAAACCTATATTTGTAGTAAGCCGGGAACCTCTGAATACCA
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA
TTAAAGATGATTACAATGAACTGTTCAAAAAAGACAGAAGTTGTGATCACATTGGATT
TCTGTATCAGAAACATTGAAAAAACTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC
TGGAAGCGGCAGAGTTAGGTGAAATTTAGACATACACACCAAATTTGTTGAGACTTTCCA
GTTCTCAGGGAACAATAGAAACAGTCTTCAGGATATCGACAGCAGATTATCTCCAGGTG
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG
AAAAACTACAAGTCTGTTAAATTGCATGACAGAGATTTACTATCAGTTCAAAAAAGACA
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAATCCACAAATTTGATAAGCAAAAAC
TGTTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTTAAAAAGTATG
AGGCATTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT
TATTATCGCTGACTAATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAT
ATACTAATGAGTTACAAGAACTCTGCCTCAGAAAATGTTTACAGCTTCCAGTGGAAATCA
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGA
TGAAGAAATTAAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA
TTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT
AGCTTTCTAATAGAAGTTTAAAGAAAAGTTTCCGTTTGCACAAGAAAATAACGCTTGGGCA
TTAAATGAATGCCCTTTATAGATAGTCACTTGTTTCTACAATCCAGTATTTGATGTGGTGC
TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTTTGGCTGCTGTGAA
GATGTAATTTTATCTTTTAAACATTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC
TAAATAAGTTATTTTCTCTGACCGCCTACTGGAAATATTTTTAAGTGAACCAAAATAGG
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAATGGTAGAACGGTGGCTAC
TGTGAGTGGGGAGCAGAACCGCACCCTGTTATACTGGGATAACAATTTTTTTGAGAAGG
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCCAGATCCCAGTTATCCTTGTATCCATG
TAATTTTACAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTA AAAACTATTC
ATTTTTTTCCTTTGGCCATAAATGTGTAATTGTCATTAAAATTCTAAGGTCATTTCAACT

FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT
CAATTTTAAAAAA

SEQ ID NO: 6_AA305176_H

TGGCTGCTCGCGGAGGGGCAGTGTACGCGGGGCGCTGTAGGCTGTCCAGCGATGGATCC
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATTAGCCG
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA
TGCCTGGCACTAAGCAAAAGCCCATTCAATTGTCCATTTGTATTATTTCACTGCAGTCTGC
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT
TATTTCTAATGAGGGTCATATTAAACTGACGGATTTTGGCCTTTCAAAGTTACTTTGAA
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA
TTATTCAAGAACCCAGGACAAGTGTATCGCTTATCAGCTCGTTGGGATTTAACACACC
AATTGCAGAAAAAATCAAGACCCTGCAACATCCTTTACGCCTGTCTGTCTGAAACATC
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA
TTCTAGCAAATTACTAAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG
TAGTCAATCCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCATAAAGAAATGAAATTGTTA
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCCTGCACATTCTGTCAAATTC
TTTTGAAATATTTCAATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA
GATTCTTGACGTAAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTTGGTTTTGTTTTATTTTGT
TTTTAACATATGTCATTTAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7_AA116841_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG
CAATGGACATGCTTTTAAACCATTTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAC
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTTCG
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCAATTTTTATCTAACTTGTGA
TATAGAATTAAGTTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAAATTACTAAGTACAACAGTTTTTACAG
AATTAATAACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAACTGTATATAA
GCCATAATAGCTTTTTTTCATCTTATTTATTCACTGCACTTTATGAAGAGCAAAGTATCAA
TAAACTAAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8_AA256100_H

AGGGAGCTGACGGGCGCCCGGCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC
TATGAGCAACCATACCCGGGAAAGAGTGACTGTAGCCAAGCTCACATTGGAGAATTTTTA
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATTAGAAGTGGC
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTGATCACAACACGCTCG
CAAAGAAACAGAGTTCTTACGGCTCAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA
GATGTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT
CTACATTTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTTTATCCATCG
GGATATTAAGCCAGACAACCTTTTTATTGGATGCCAAGGGTCATGTAAATTTATCTGATTT
TGGTTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA
CAACCCACCAAGTGACTTCTCATTTTCAGAACATGAACTCAAAGAGGAAAGCAGAAACTTG
GAAGAAGAACAGGAGACAACCTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC
AGAAGTATTTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA
CAGAAAAGTGATGAACTGGAAAGAAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA
GAAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAACAGAATTGGAAATAG
TGGAGTAGAAGAAATAAAAGGTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA
TGACTTCCCTGAATCTGATATTTTACAACCAGTGCCAAATACCACAGAACC GGACTACAA
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC
TGAAATACTCCTGAAGATGGTGGTGCCTATTGACTACAAGAGGAAATTTCTACAGGATTAG
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAATAT
TTTATTATTTTTGTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT
TTGAACTGTAACACCTCTAATCAATTCAGGAGAAACACATATCATTAAAGCAACATAGG
CTAACCTGTAGGTAACACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTTAGAACATTGCCCTATTGGTTTGGACATC
TGTAGAATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAACTTCACAGTAAGGAG
TGACAAGTTTTATAATAAGGAAGACAAAGTTTAACACCTTCACTCAAGCACTCCACTAATA
TATTTACGTTGCATTACAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGA ACTTCTT
TTTTTAACAAGAGGACATGGCATTATTTTAATTTGATTATGGTGAGTTGAATTTAAGACA
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTTATTAACTATTTTTTTTAAATGTC
AACTTCTATCATGTAAATGGACTTATAGAGAACA AAAAGCTATTTACTTTGGTTTTCTA
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTTCTTTTGATGAAATTTTTCTCTT
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAGATCTT
GAACAGAGTGGATGTTTACAACTGAGTAGAATTTTCTTTCTGTGGGCATGCTGTATTCT
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAAGGGCAATATTGTTCTTGTTTAG
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTTGT
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATCTTTGGGTATCTCTCTAAGAATT
AAATAATCTTTTCTAGCTTAATATTTTAATTCTAATTCAAACAACTCTGAGGTTTTGGTT
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAATGGCCTAATGTTTGTCTATAAC
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTTATAAATGATCTATGA
TCAAAATCTAAAGTGATGAATTATTTGTAGGAATGTCTTCCTAATGGGGGAAGAATTGCAT
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG
TGTTTCATAAGGCCATCCTGTTTCCCCCACTCCCCCATTTTTTGGTTTTGTTTCTTTTTAA
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACTTCCATTTTTCTAGTCTGGAT
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAACTCTGGGGATTTCTCAATGTGACTAA
CTCTAATTTTTCTAATTATACTGCCTTTAATTAACATAATATTA ACTTTTGCTGAGGTT
TATGAGATTTTCTCACCACATCGCTCCCCTTTTTTTAAAGGACTGTTTGTCTAGTG
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCTAGTTCTAGTATGGTAA

34/113

FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA
GAAACTGATTTACCTAAGTTTACTTTTTTAATTGCATAATAGAGCATTTTTTTGTTTTGAGT
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTACTTTCTTGGCACTGGAAG
GGTAGTTCTGGAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAAGCATTTCCTTAAGTGCCTATCTAAAAGC
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTCATGATGCAAATTAAC
AGATAATTTGCAAAGTACCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTT
AGGTGAATAATTTAATTTAAATGACAAAACCTTATCTAGTCAACTGGGCATAATGACATT
TTCTTTAAATTAGACTCTATTTTGAATTAAAAGAGTTTTATTATAAACCGTGTGTTTTTG
GTTTTTCTAAGTATATAGAAAGCTTGTATAATTCAGATTTATCAATTTTCTGATTTAATG
TAGACTTTGACTTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT
GAAAATAAGGAATTGCTTATAAACCAGCCACTTCTGAATACAATATGTAGCTGATTTAAT
AAGCTAGTTAGTGAATGGAAAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT
TTTATGTAAATCTCTAAATTTAAATATTTTAAGTACATTTATTTTTGGTGTTTTATTGT
ATAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA
ACACATTCTCCTTTGAATTGTTAAATTCAGAACATTCAAATAACTGTTTTGCTACAAC
CCATGATTATTTTCTGTTGTGTTTTATTTAAATTTACTTTCTCTTTAGAAGTGCATTAT
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA
CTACTAGAGATATTTTAGATTTTATGAAAAAATGTGAGGGGATATTGCTGCTTTAAAA
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTTAAAGCAATATAATTCAGCAAT
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTTCAAGTTACTGAGTTTCAAAAA
TGTTTTGGTGGCATGAGGACAAAATTTCAATTGAAGGTAAGATAAGAATAAAAACTATGTT
TAC

SEQ ID NO: 9_AA210825_H

CACGAGGGCTACTGGCGCCTGGCGACCCCTCCCTGCCCCCACCCAACCCCGCTCCGGCAA
CGCCCCCTTCTCACGGCTCCCGACCGAACTTTTCTCCAACCTCTGCGACTCGTGAGATT
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCATCCCCTGGCCGGTCCGGTCCC
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA
CCCCAAGGACCCCGCCATCCTCAGGTCCCCTCCGCCTGCCAGATCTTTTCTCGGATCCC
CGCTCTCCACCACTGCTCACGAGATCCCGCGGATCTAGAACCCAGGGTCCCCCGGGG
CCCCCGGCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCCTCCCCCATGGCCAC
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGGTCTCCTCCGCCCC
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGTACTGCCCCAGATCCCGGCCCCGGGTT
CCGGGGTCTCCTTTCACATCCAGATCGGGCTGACCCGCGAGTTTCGTGCTGTTGCCCGCCG
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGAGACCAGAAGTTCCTTG
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTCAAACATGACCCACGTCGG
CCAACCTCCTGCAGCTGGTGCGCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG
TGGTGCTGTCGGCCTCGGCCACCTTCGAGGACTTCAGATCCGCCCCGACGCCCTCACGG
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG
TGCGCCAGGGCCTCAAGTGCGATGGCTGCGGGCTGAACTACCACAAGCGCTGTGCCTTCA
GCATCCCCAACAACCTGTAGTGGGGCCCGCAAACGGCGCCTGTCATCCACGTCTCTGGCCA
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA
GCCGTAGCACCACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCTCCTCTTCTG
CCTCATCGTATACGGGCCCGCCCCATTGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG
TGCCGCACACCTTCTCATCCACAGCTATACACGGCCACCGTTTGCCAGGCTTGCAAGA
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGTT
GGGTGGTTTCAATTACAGCAACAAGGACACGCTGAGAAAGCGGCACCTATTGGCGCCTGGACT
GCAAGTGTATCACGCTCTTCCAGAACAACACGACCAACAGATACTATAAGGAAATTCCGC
TGTCAGAAATCCTCACGGTGGAGTCCGCCAGAACTTCAGCCTTGTGCCGCCGGGCACCA
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG
GCGGGACTCCGGGTGGGCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA
CAGCCATCCGCCAGGCCCTGATGCCCCGTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGGGACGTGGCAGTTAAGGTCA
TTGACAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTTCGAGACGCCTGAGA
AAGTGTGTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG
AGAAGGGCCGGCTGCCTGAGCGCCTCACCAAGTTCCTCATCACCCAGATCCTGGTGGCTT
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC
TGGCATCAGCAGACCCATTTCCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA
TCGGCGAGAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCACTGGGCGTGATCATGT
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC
AGAACGCCGCCTTCATGTACCCGGCCAGCCCCTGGAGCCACATCTCAGCTGGAGCCATTG
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA
AGATGGGAGAGCGATACATCACGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGACG
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCACGGACAGGGATCTCGGTGGGGCCTGTC
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTTCTCTGAGGTCCTG
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTACAGGATCCCAGCAATGAACTG
TTCTAGGGAAAGTGGCTTCCCTGCCCAAACCTGGATGGGACACGTGGGGAGTGGGGTGGGG
GAGCTATTTCCAAGGCCCTCCCTGTTTCCCCAGCAATTAAAACGGACTCATCTCTGGCC
CCATGGCCTTGATCTCAGCAAAA

SEQ ID NO: 10_AA127299_H

ATTCAATTCATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT
GATCCTTACATCAAAATCACAAATCTTTCTCAAAAAACGAAAGTGATTAAGAAAACTTTG
ACTCCAACCTTGAATGAACTTTTTTTGTGCATTTTCCAGAAAAACAACCCTTGAATTA
GAATGTTGGGACCACGATACTTTTTTTCAGATGATTTTATTGGCAAGGCTTCCATTTCTTTG
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAAGGA
GAATTTGCAGGAAAA

SEQ ID NO: 11_AA316804_H

ATGTCTGCAATAATTCCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCCT
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCCTAAGACGGGACTCTCTGCCCGACTC
TCTAATGGAAGCTTCAGTGACCATCACTCACCAACTCCAGAGGCTCAGTGACATACAGTT
TCATTTCTACTGCAAAATGGCCTCACACGGGAGAGTGTTACCATTTGAAGCCAGGAACTG
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT
GGATTCTTTGGCATGTATGACAAAATTCTTCTCTTTCGCCATGACATGAACTCAGAAAAC
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

36/113

FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTTCGTCCACATACTCTCTATGTACAT
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT
CCAAATAACTGTAGTGGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA
CATGTCCACCAGGAACCAAGTAAGAGAATTCTTTCTTGGAGTGGTCGCCCCAATCTGGATG
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTTCGCCAAGGAATG
CAGTGTAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCTTCCAGTCTGGGAACAGATACAGATATA
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAAATGGTGAAGGAA
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT
GACAGCAAATGTCTAACATTATTTTCAAGATGAATCTGGATCAAAGTATTATAAGGAAATT
CCACTTTTCAAGAAATCTCCGCATATCTTACCACGAGATTTTCAAAACATTTTCAAGGC
AGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATACTTTCGTTGGTGAGAAC
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA
CAGAGCTGGGAAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT
TGCATTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT
AATTGTCAGATTCAGGAGAATGTGGATATCAGTACTGTTTACCAGATCTTTGCAGATGAG
GTGCTTGGTTTCAGGCCAGTTTGGCATCGTTTATGGAGGAAAACATAGAAAGACTGGGAGG
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT
ATGTTTGAACCCCAAGACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC
ACACAGATACTTGTGCTTTGAGGAATCTGCATTTTAAAGAATATTGTGCACTGTGATTTA
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCTCAGGTGAAGCTGTGTGAC
TTTGGATTGTGACGCATCATTGGTGAAGAGTCATTTCAGGAGATCTGTGGTAGGAACTCCA
GCATACTTAGCCCCGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCTTTTAAATGAGGATGAA
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA
ATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC
CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGATGCT
CGCTGGGAAATACATGCATACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT
CCTAATCCAGATGATATGGAAGAAGATCCTTAA

SEQ ID NO: 12_PKNBETA_H

ATGGAGGAGGGGGCGCCGCGGCAGCCTGGGCGGAGCCAGTGGCCCCCAGAGGATGAGAAG
GAGGTGATCCGCCGGGGCCATCCAGAAAGAGCTGAAGATCAAGGAGGGGGTGGAGAACCTG
CGGCGCGTGGCCACAGACCGCCGCCACTTGGGGCCATGTGCAGCAGCTGCTGCGGTCTCTCC
AACCGCCGCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCCGAATCCTGCTG
CCCGGCCCTGGGCCTGGCCCAGCTGAGCCTGTGGCCTCAGGACCCCGGCCGTGGGCAGAG
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCCAAGGAGAGGAAG
CTCCTTGCAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGGAGCCAGGGCCTGAGCTACTGGCG
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAACGTG

37/113

FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCCAGGCC
CAGCTACAGGAGTCCTCTCAGAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG
GAGCAACTGCCTCCTGCCCACCCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCCACCGCCCTAACAGGGACA
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA
GCGGCCGCACTGGCCAGCAGCCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT
GTGGGGCAGACGGGCTGGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTCAATC
CCACTGGAGCGAGCCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA
TGTGGCGTGGCCTTCCTGAGACTTGAAGACTTCCTGGACAATGCCTGTCACCAACTGTCC
CTCAGCCTGGTACCGCAGGGACTGCTTTTTGCCCAGGTGACCTTCTGCGATCCTGTCATT
GAGAGGCGGCCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC
TTCTTGAGGCGTTTCGAGATGAACCTCGGCATGGCGGCCTGGGGGCGCCTCGTCATGAAC
CTGCTGCCCCCCTGCAGCTCCCCGAGCACAAATCAGCCCCCCTAAAGGATGCCCTCGGACC
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCCAGTAATTTCTGCCCCAAGAAG
ACCCCTTGGGTGAAGAGATGACACCCCCACCCAAGCCCCCACGCCTCTACCTCCCCCAG
GAGCCAACATCCGAGGAGACTCCGCGCACCAACGTCCCCATATGGAGCCTAGGACTCGA
CGTGGGCCATCTCCACCAGCCTCCCCCACCAGGAAACCCCTCGGCTTCAGGACTTCCGC
TGCTTAGCTGTGCTGGGCCGGGGACACTTTGGGAAGGTCCTCCTGGTCCAGTTCAAGGGG
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCT
TTCCTGCTCTCCCTCCTTGCTGCTTCCAGACCTCCAGCCATGCCCCGCTTTGTGACTGAG
TTTGTGCTGCTGGTGACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG
GCCCCGCTTCTACGTGGCTTGTGTTGTCTTGGGGCTGCAGTTCTTACACGAGAAGAAGATC
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCCAGGGATTCTTGAAGATC
GCAGACTTTGGACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT
GGCACCCCGGAGTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACAGGCCGTC
GACTGGTGGGCGCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA
GGGGACACAGAGGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCCGGC
TTTCTGTGCGGTGCAAGGGCTTGAGTTCATTTCAGAAGCTCCTCCAGAAGTGCCCGGAGAAG
CGCCTCGGGGCAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC
ACCAACTGGCAAGCCCTGCTCGCCCGCACCATCCAGCCCCCCTTCGTGCCTACCTGTGT
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACC
CCACCTGCACCCACAGCCTCCTACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGAC
TTTGTGTGAGAGCGATTCTTGAACCCCTGA

SEQ ID NO: 13_AI021023_M_PKNBETA_M

GCTGAAGTGGGATAACCTTCTGCTGGATGCCCAGGGATTCTTGAAGATCGCAGACTTTGG
ACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGTGGCACCCCGGA
GTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACGGGCTGTGGACTGGTGGGG
GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA
GGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCCGGCTTTCTGTGCGT
GCAAGGGCTTGAGTTCATTTCAGAAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGG
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA
AGCCCTGCTCGCCCGCACCATCCAGCCCCCCTTTGTGCTTACCTGTGTGGCCCTGCGGA
CCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACCCACCTGCACC
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGACTTTGTGTGTCAGA
GCGATTCTTGAACCCCTGAGGGCATCTCCTGGCACCTCTGTCCCCCTTCCCCACAGACTG
TTAGAGCCTCTGCTCGTTACCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA
GACCTGGCCCAGAAAGGGTGCCGCAGCAAGGAGTGATATGGTTTGTCTTTTAAAGACTGG
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14_H19102_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA
ACCATCAGGTCAGATCTGGAAGAACTCTGGGAACACGGGGGCACCACTATCTGCACCAG
GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGGCCAGTGCCT
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG
CTGAAGATTTTAGGCCCTCGTGGCTAAAGGCTCCTTTGGAAGTGTCTCAAGGTGCTAGAT
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCAAGGTAAAGGTCTTACAGAGG
GATACCGTGAGGCAGTGCAAAGAGGAGGTTAGCATCCAGCGACAGATCAACCATCCCTTT
GTACACAGCTTGGGGGACAGCTGGCAGGGGAAAACGGCACCTTTTCATTATGTGTAGCTAC
TGCAGCACAGATCTGTACTCCCTTTGGTTCGGCTGTTGGCTGCTTTCCTGAGGCTTCCATC
CGTCTCTTTGCTGCCGAGTTGGTGTCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG
CATCGAGATGTGAAGATGGAGAATATCTTCTAGATGAACGAGGCCATCTGAAACTGACA
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT
CTTCAGTACATGGCCCCAGAGGTCCTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGCGCACTGGAAAGTTTCCAGTGGCTGCAGAG
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGAAGTCTGAGATCCAGCTTCT
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCCCTCCATCGT
CTACGTTATCTGCATCACTTCCAGGTCCACCCTTTCTTTTCGGGGTGTGGCCTTCGACCCA
GAGCTCCTACAGAAGCAGCCAGTGAAGTTTGTACGGAGACACAAGCTACCCAGCCAGT
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC
CCTATCCCTGCTTGA

SEQ ID NO: 15_AA476563_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAAGTCTTGGGACTTGACTTT
GGAGAAAAATTGTATAGTCTAAAATCAGAACCTTTGAAACCATTTCTTTACTCTTCCAGAT
GGAGACAGTGCTTCTAGGAGTTTTAATACTAGTGAAAGCAAGGTAGAGTTTTAAAGCTCAG
GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTTCGTTTAAAGATGCTGCT
TTTGATGATGTCAAGTGGTACTGATGAAGGAAGACCTGATCTTCTTGTAATTTACCTGGT
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAACTAAT
ATAGGGATAATAGAAAATAAACTCTTGGAAAGCCCCTGATGTTTTATGCCTCAGGCTTAGT
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAAGTGAAGTATCCCTCTGGG
CCCAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT
GTAGCAGCTGTTGATCATAGTAGTTCAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
TTATTCCGTATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTTGGCTAAAGAGGAA
CCAACCTCTTTATTCCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA
GGAGACAAGGAAATACATCAGATTTTTGAGGACCTTGATAAAAAATTAGCACTAGCCTCC
AGGTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT
GATGCTTTACATAGAGAGGGAATTGTGTGCCGCGATTTGAACCCAAACAACATCTTATTG
AATGATAGAGGACACATTCAGCTAACGTATTTTAGCAGGTGGAGTGAGGTTGAAGATTCC
TGTGACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTGGAGCAATCACTGAA
GAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCTCTTTGAACTTCTCACTGGC
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAAGTTCAATCCTCTG

FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTGAAGATATCAAATCTCATCCATTTTTTACC
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16_AA626690_H

ATGCTACCATTCGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTTCAGCGGC
GGCGGCGCGAGCAGCGGCGAGGTAAATGGTCTTAAATGGTTGATGAGCCAATGGAAGAG
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT
CAGGGGTCAATTTGGAAAGGTTTTCTTGTTAGAAAGAAGACCGGTCTGATGCTGGGCAG
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTAAAGTTTCGAGACAGAGTTTCGGACA
AAGATGGAGAGGGATATACTGGTGGAAGTAAATCATCCATTTATTGTCAAATTGCACTAT
GCCTTTCAGACTGAAGGGAACTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATTCTACCTCGCA
GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT
GTTCTTATGTTTGAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG
ACCATGAATATGATATTAAGCAAACTTGAATGCCTCAATTTCTTAGTGCTGAAGCA
CAAAGTCTTCTAAGGATGTTATTCAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA
GTTGAAGAAATCAAAAGACATCTGTTTTTGC AAATATTGACTGGGATAAATTATATAAA
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGAAAACCAGATGATACTTTTTGTTTT
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAT
GCTCATCAGCTCTTCAAAGGATTCAGCTTTGTTGCAACTTCTATTGCAGAAGAATATAAA
ATCACTCCTATCACAAGTGCAAAATGTATTACCAATTGTTTCAGATAAATGGAAATGCTGCA
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGGCTCCTACTCTGTTTGC
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAATGTTTCTCGGAACGGGAGGCT
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGCAGATTCA
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAATGGACTTCTCTTA
ACTCCATGCTACACTGCAAACTTTGTTGCACCTGAGGTTCTTATGCAACAGGGATATGAT
GCTGCTTGTGATATCTGGAGTTTAGGAGTCCTTTTTTACACAATGTTGGCTGGCTACACT
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA
AAATTCTCTTTGAGTGGTGGAACTGGGACAATATTTTCAGACGGAGCAAAGGATTTGCTT
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCCAGCGACGGAGCATGAAAAAGCGA
ACATCAACTGGCCTGTAA

SEQ ID NO: 17_AA215680_H

ATGAGCCTGGTGGCCTGTGAGTGCTGCCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTCGCAACAGGGTGGCTCTGGGA
GTGCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC
CTGGAGCGCGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG
GACGTGCTGCTCCGTGGCATAACGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG
CTGAAAATTACCAAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGCGGGTTTCAGCAGCCTGAGGCTCCGGGCCATT
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTCATCGAG
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC
AGGTGCCACATGGTGAGCAGGGAGCGGCTGACCATCATCCCACACGGAGTCCCCTACATG
ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCTGACCTGGAGCATGTG
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG
ACCCAGCGAGGCTTCCCTCAGGCCATGCCCTGGCCAGGACAGAATCGCCCTGGAGCCT
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACCAGACCCAGAGG
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG
CCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG
CCCCCTCGGGGGCTCACTTGGGTTCCTGAGGGGGCCGGCCCGGTGCTAGGGGGCTGTGGC
CGAGGCATGGATCAGAGCTGCCTGTGAGCAGATGGGGCCGGCCGGGGCTGTGGCAGGGCC
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG
GAGGCGCTGCACGAGCAGGGGGTGTGTGCCGGGACCTCCACCCCGGGAACCTGCTCCTG
GACCAGGCAGGTACATCCGGCTCACATATTTTGGCCAGTGGTCAGAGGTGGAGCCCCAG
TGCTGCGGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA
ATGGCACTGTCCCAGAGCCACCTTCAGGAATCCAGGCCACACCCAGCTCCAGCTGCCC
GAGTGGCTCAGTCGCCAGCGGCCTCTCTGCTGACTGAGCTGCTGCAGTTTCGAGCCTACC
CGGCGCCTGGGCATGGGAGAAGGTGGTGTGAGCAAACCTCAAGTCCCATCCCTTTTTTCAGT
ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18 SGK_H

ATGACGGTGA AAACTGAGGCTGCTAAGGGCACCTCACTTACTCCAGGATGAGGGGCATG
GTGGCAATTCTCATCGCTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAG
AAGATTGCCAATAACTCCTATGCATGCAAACACCTGAAGTTCAGTCCATCTTGAAGATC
TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCTTCTCCTCCACCAAGTCCTTCT
CAGCAAATCAACCTTGGCCCCGTCGTCCAATCCTCATGCTAAACCATCTGACTTTCACTTC
TTGAAAGTGATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCAGAA
GAAGTGTTCTATGCAGTCAAAGTTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG
AAGCATATTATGTGCGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCTTTTCTGCTG
GGCCTTCACTTCTCTTTCCAGACTGCTGACAAATTGTACTTTGTCCTAGACTACATTAAT
GGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCACGGGCTCGT
TTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTAT
AGAGACTTAAACAGAGAATATTTTGCTAGATTACAGGGACACATTGTCCTTACTGAT
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAAATCCACCTTCTGTGGCAGC
CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGG
TGGTGCCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCCTTTTTATAGCCGA
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT
ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTCCTTAATTAAGTGG
GATGATCTCATTAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCCAAC
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCCAACTCCATTGGCAAG
TCCCCTGACAGCGTCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCCTAGGC
TTTTCTATGCGCCTCCCACGGACTCTTTCCTCTGA

SEQ ID NO: 19 AA107515_M

CGGGTCGACCCACGCGTCCGCCGGTTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCTTACCTACTCCA

FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCCTGA
ACGATTTTATTTCAGAAGATTGCCAGCAACACCTATGCGATGCAAACACGCTGAAGTTCAGT
CCATTTTGA AAAATGTCCCATCCTCAGGAGCCGGAGCTTATGAACGCTAACCCCTCTCCTC
CGCCAAGTCCCTCTCAACAAATCAACCTGGGTCCGTCCCTCCAACCCTCACGCCAAACCCT
CCGACTTTTACTTCTTGAAAGTGCATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTGGCTA
GGCACAAGGCAGAAAGAAGTATTCTATGCAGTCAAAGTTTTACAGAAGAAAGCCATCCTGA
AGAAGAAAGAGGAGAAGCATATTATGTGAGAGCGGAATGTTCTGTTGAAGAATGTGAAGC
ACCCTTTTCTGGTGGGCCCTTCACTTCTCATTCAGACCGCTGACAAGCTCTACTTTGTCC
TGGACTACATTAATGGTGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCCTGG
AACCACGGGCTCGATTCTACGCAGCTGAAATAGCCAGTGCCCTGGGCTATCTGCACTCCC
TAAACATCGTTTATAGAGACTTAAAACCTGAGAATATTCTCCTAGACTCCCAGGGGCACA
TCGTCTCTCACTGACNTATTTAGCTGCGTAGAATCGAGCATAACGGGACAACATCTACCT
TCTGTGGCACGCCTGAGTATCTGGCTCCTGAGGTCTCCATAAGCAGCCGTATGACCGGA
CGGTGGACTGGTGGTGTCTTGGGGCTGTCTGTATGAGATGCTCTACGGCCTGCCCCCGT
TTTATAGCCGGAAACACGGCTGAGATGTACGACAATATTCTGAACAAGCCTCTCCAGTTGA
AACC AAATATTACAAACTCGGCAAGGCACCTCCTGGAAGGCCTCCTGCAGAAGGACCGGA
CCAAGAGGCTGGGTGCCAAGGATGACTTTATGGAGATTAAGAGTCATATTTTCTTCTCTT
TAATTAAC TGGGATGATCTCATCAATAAGAAGATTACACCCCATTTAACC CAAATGTGA
GTGGGCCCAGTGACCTTCGGCACTTCGATCCCGAGTTTACCGAGGAGCCGGTCCCAGCT
CCATCGGCAGGTCCCCTGACAGCATCCTTGTCACGGCCAGTGTGAAGGAAGCAGCAGAAG
CCTTCCTCGGCTTCTCCTATGCACCTCCTGTGGATTCTTCTCCTCTGAGTGCTCCCGGGAT
GGTTCCTGAAGGACTTCCTCAGCGTTTCCTAAAGTGTTTTTCGTTAGCCTTTGGTGGAGTTG
CCAGCTGACAGAACATTTTAAAGAATTTGCACACCTGGAAGCTTGGCAGTCTCGCCTGC
CCGGCGTGGCGCGACGCAGCGCGCGCTGCTTGATGGGAGCTTTCGGAAGAGCACACCCTC
CTCTCAATGAGCTTGTGAGGTCTTCTTTTCTTCTCTTCTTCCCTTCCAACGTGGTGCTAGCTCC
AGGCGAGCGAGCGTGAGAGTGCCGCTGAGACAGACACCTTGGTCTCAGTTAGAAGGAAG
ATGCAGGTCTAAGAGGAATCCCCGCAGGTCTGTCTGAGCTGTGATCAAGAATATTCTGCA
ATGTGCCTTTTCTGAGATCGTGTTAGCTCCAAAGCTTTTTCTATCGCAGAGTGTTCAGT
TTGTGTTTGTGTTGTTTTGTTTTGTTTTGTTTTGTTTTTCCCTTGGCGGATTTCCCGTGTGTGCA
GTGGCGTGAGTGTGCTATGCCTGATCACAGACGGTTTTGTTGTGAGCATCAATGTGACAC
TTGCAGGACACTACAATGTGGGACATTGTTTTGTTTTCTTCCACATTTGGAAGATAAATTTA
TGTGTAGACTGTTTTGTAAAGATATAGTTAATAACTAAAACCTATTGAAACGGTCTTGCAA
TGACGAGCATTGAGATGCTTAAGGAAAGCATTGCTGCTACAAATATTTCTATTTTTTAGAA
AGGGTTTTTATGGACCAATGCCCCAGTTGTCAGTCAAAGCCGTTGGTGTTTTCATTGTTT
AAAATGTCACCTATAAAAACGGGCATTATTTATGTTTTTTTTTCCCTTTGTTTCATATTCTTT
TGCATTCTGATTATTGTATGTATCGTGTAAGGAAGTCTGTACATTGGGTTATAACACT
AGATATTTAAACTTACAGGCTTATTTGTAAACCATCATTTTAATGTACTGTAATTAACAT
GGGTTATAATATGTACAATTCTCTCTCTTACCACACAACCTTTTTTTGTGTGCGATAAAC
CAATTTTGGTTTGCAATAAAATCTTGAAAAC T

SEQ ID NO: 20 AA109508 M

CCACCTGCAGCGGGAGCGCCGGTTCCTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGT
GGCCAGCGCCATTGGCTACCTGCACTCCCTCAACATCATTTACAGGGATCTGAAACCAGA
GAACATTCTCTTGGACTGCCAGGGACACGTGGTGTCTGACGGATTTTGGCCTCTGCAAGGA
AGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACCCCTGAGTACTTGGCACC
TGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGCTTGGGGGACGT
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCAGATGTA
TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGA
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTT
TCTTGAGATTAAGAACCATGTATTCTTCAGCCCCATAAACTGGGATGACCTGTACCACAA

42/113

FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGA
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC
CAGCAGCTCTGGGGCCTCAAGTGCATTCTGGGATTTTCTTATGCGCCAGAGGATGATGA
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAACTACTGAGGCCAGCTGGTATTAGTA
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAACCTAACAAATGGCTTCAACGAGAAG
CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT
CCAATGTTAGGTTTGCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAG
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAA
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTT
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG
CCTCCTGGTGTGTTGGATTTTGATCTCAATGTGTAAAATGACAGAGATGTAACAAGCTCAT
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21_AA887783_H

CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT
ACAAGGAAAGCTGCCCAAGTGTAAGNATTCCCAGCTCCGATGAACACAGAGAGAAAAAGA
AGAGGTTTACTGTTTATAAAGTTCTGGTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAACAGTTTCCTGCTANGG
CCCTGAAGATTTCCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAAC
AAAGACGAGCAGGACTAAACGAATTCATTCAGAACCTAGTTAGGTATCCAGAACTTTATA
ACCATCCAGATGTCAGAGCATTCCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCAT
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAACATCAACC
TGGGACCGTCTGGAATCCTCATGCCAAACCACTGACTTTGATTTCTTAAAGTTATTG
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAAACGGAACTGGATGGAAAATTTTATG
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAGAGCAAAAACATATTATGG
CTGAACGTAATGTGCTCTTGAAAAATGTGAAACATCCGTTTTTGGTTGGATTGCATTATT
CCTTCCAAACAACCTGAAAAGCTTTATTTTGTCTGGATTTTGTTAATGGAGGGGAGGGAC
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA
CCACATTTTGTGGGACACCAGAGTATCTTGCACCTGAAGTAATTAGAAAACAGCCCTATG
ACAATACTGTAGATTGGTGGTGCCTTGGGGCTGTTCTGTATGAAATGCTGTATGGATTGC
CTCCTTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG
ACAGGCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAATCATCCTTTTT
TTGAATCACTCAGCTGGGCTGACCTTGTAACAAAGAAGATTCCACCACCATTTAATCCTA
ATGTGGCTGGACCAGATGATATCAGAACTTTGACACAGCATTTACAGAAGAAACAGTTC
CATATTCTGTGTGTGATCTTCTGACTATTCTATAGTGAATGCCAGTGTATTGGAGGCAG
ATGATGCATTCGTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTTGTGAGCAG
TTTGCCATTACAGAAACCATTTGAGCAAAATAAGTCTATAGATGGGACTGAACTTCTATTT
GTGTGAATATATTCAAATATGTATAACTAGTGCCTCATTTTTTATATGTAATGATGAAAAC
TATGAAAAAATGTATTTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT
TGATTAAAATTTATATTCTTGTTTAAATAAGCTTATTTTTTAAACAATTTAAAAGCTATTAT
TCTTAGCATTAACCTATTTTTTAAAGAAACCTTTTTTGTCTATTGACTGTTTTTCCCTCTA
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTTAACAGTCAATTTAGTTTACGCT
AACATATATTAATACCTTTGTAACCTTTGCTATGGCTTTTGTATCACACCAAAACTAT
GCAATTGGTACATGGTTGTTTAAAGAAGAAACCGTATTTTTCCATGATAAATCACTGTTTG
AAATATTTGGTTCATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG
TTAACAATTGGAATAACTTTATTTCTGCAGATCATTTAAGAAGTAACAGGCCGGGCGCGGT
GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCA

43/113

FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT
TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA
ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG
CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22_R47805_H

ATGGCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA
CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT
GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGCTGCTGCCACTG
CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGC
TTCGAATGGCTCTTCCTCGCCTGGTCGCCTGATAACTCCCCCGTGCGGCTGAAGATGCTG
TACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCCACATCAAGGATGAG
CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGGTGGGTACCAGAAACACCTGTCGTCC
TGTGCGGCACCTGCCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC
GAGGTGAAGACAGAGATCAGTGTGGAAGCAAGCACCAGACCCTGCAGGGCCCTCGCCTTC
CCCCTGCAGCCTGAGGCCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC
ATCCAGATGAAGCTGGACCTAGAGCGGGAAACCATTGAGCTGGTGCACACAGAGCCCACG
GATGTGGCCAGCTGCCCTCCCGGGTGCCCCGAGATGCTGCCCGCTACCACTTCTTCCTC
TACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTTCATCTACTCCATGCCG
GGGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTC
GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG
GCAGAGCTGACGGCAGAGTTCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG
CAGGCCTTCGCCAAGCCCAAGGGCCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCGC
GGCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23_H60215_H

CCACGCGTCCGGCGCCGAGCCATGGAGGGAGGCGGCGGGCGGCGGGCGGCGGCTCGGG
TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCTCCAGCCCGGCCCCGGCCCC
CGGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA
CCACCCGGCGAAGTGCACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTACAGC
ACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG
CACCAGGTCTGAATTCCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT
GACCACAGACCCATTCCAGGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA
TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCA
GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAATAATGCAAAGAGAGCTGGACCATTCA
TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAGTGCAAGTGTGGCGAGGA
AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC
AAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTCAC
TGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACC
GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC
GCATCTGCCTCGTCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC
TCATCAACCTGCAGCACTACGTCTATCAAGGAGAAGAGGCTCAGCGAGAGGGGAGACTGTGG
TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCACA
GAGACCTGAAGCTGGGGAAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCA
ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA
GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCCGCCGTACCGTGGCAAGCCCAGTG
ACATGTGGGCCCTGGGCGTGGTGTCTTACCATGCTGTATGGCCAGTTCCCTTCTACG
ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGAGG
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGGACCCCC
AGCAGCGCCTGGCCGCCGCCGACGTCCTGGAGGCCCTCAGTGCCATCATTGCATCATGGC

FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCAGTACGAGTTTG
AGAACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC
GGAGCTGGGTACCCAAGCGGCAGTTCGGCAGCGCACCACCGGTGCGACGGCTGGGCCACG
ACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG
TGGCTGTGAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC
AGGGACAGGGACAGCCCAGGTACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT
TGGGATGATTGCTCGATTGTTTGGTTTTTAAATCTGAGAAGCCTAGATAACTAATCTGCT
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC
AAGAGGGAGGAGGGAGCCTGCTCACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTG
ACCTGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGCAGCTCGCTGCAGGCCCC
AGAGCGAGCTTCCCCTCCTCCCTGCTCTCCAGGCCCTGCCACAGCCTCTTTCCGTCCC
TCTCTTTCTGATCCAGGCCCCCTCAGTCCAAGCTTTGGAAAACCTTCACCTCATCTTAAAC
CAAACCTCAAATATATTTATTTTTTTTACCAT

SEQ ID NO: 24_SGK324_H

GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAGG
CCGCGGCCGGGGTTCGCGGAGAGGGGCCCCAGCTCCTCCGGGGGCAGCAGCAGCTCGGGC
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC
ACGCGGACCCCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG
AACGGGGACCGCTACTTCAAGGGCCTGGTGTTTGCCATCTCCAGCGACCGCTTCCGGTCC
TTCGATGCGCTCCTCATAGAGCTCACCCGCTCCCTGTCCGACAACGTGAACCTGCCCCAG
GGTGTCGCGCACTATCTACACCATCGACGGCAGCCGGAAGGTCAACAGCCTGGACGAGCTG
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTCTGTAAAGTCGATTACACC
AAAAATATTAATCCAAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT
GCTGCCCTCCTCTGTGAAAAGTGAAGTAAAAGAAAGTAAAGATTTTCATCAAACCCAAGTTA
GTGACTGTGATTTCGAAGTGGAGTGAAGCCTAGAAAAGCCGTGCGGATCCTTCTGAATAAA
AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC
TCAGGAGTCGTCAAGAGGCTCTGCACCCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG
CATCTGCCAGACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTT
CGTTATGCCCAAGATGACTTTGTCTTGGATCATAGTGAATGTCGTGTCTGAAGTCATCT
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC
CGTTGCATAAGTCCTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT
GAGAAATACAAAATTGGAAAGGTCATTGGTGATGGCAATTTTGCAGTAGTCAAAGAGTGT
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT
ATCATTATGCTGGTCGAGGAGATGGAAACAGCAACTGAGCTCTTCTGGTGATGGAATTG
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTGACCAAGTACACTGAGAGAGAT
GGCAGTGCCATGGTGTACAACTTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG
TCTTTGAAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTCTGTGGATTTCCACCATTC
CGAAGTGAGAACAAATCTCCAGGAAGATCTCTTCGACCAGATCTTGGCTGGGAAGCTGGAG
TTTCCGGCCCCCTACTGGGATAACATCACGGACTCTGCCAAGGAATTAATCAGTCAAATG
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG
TCAGATGATGCCTCCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAACAG
CACTTTAATAATGCGCTCCCCAAACAGAACAGCACTACCACCGGGTCTCCGTCATCATG

45/113

FIGURE 2R

GTGAGTGGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCTTCCGTAGTCCTATTTTCATATGA
AGATTGGCTTGGCATGTGGAGGGCACTCATTCGGCAACTCCCAGGCTTTGGGCACTGTGT
GGAGGGGCTTGTGTAGGGACCAGCAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC
CTGGCTGGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACCTCCCTGCCTACCCCAAGGCC
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA
AAGCTAAACATATTTTCAGTTTTTAAAAAATCAGTGTTTTTATAAAACACAGTTTGGGGCTTT
TAAAGGTACATAATCAAGGAAAAAATATATATTCAATTTTTTCAGGGTTGGTAACATTTTA
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT
TCTTAAGGCAACTCTCCTAAATACATAAACACAACAAATTAATAAGTGAAGTACATGAG
AGTAAATGAATCAAAAGGAAAAAACATTGAACCAGAGGTGAGGGCAGCACACCCGCAGCA
GCTGTCCAGGCCTGAGCCAATGCAACCCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG
GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTCGAATCA
GACCTGCCAAGGTGATGGGCGTCTGAGTTTCACATCTGGGCCCCCGTGACCCCACTGAG
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCACTCGTACTTGGGACAGGCCT
CTCATCCTCTGGGAAGGTCTCCTTGTTCCTACCCAACTAGAAGGGAAACAGTGGCATA
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA
GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCCACACTCC
CCACACCCCCCACACCCCCACATCCCCACCATAATTACCCCCACCTCCAAATATCTCAT

SEQ ID NO: 25_W30246_M SGK324_M

ACCAAGTCCTCCAGCTCCTCTCCAACCAGCCCGGGAAGTTTCAGAGGATTGAAGATTTCT
GCTCAGGGCAGATCTTCTTCCAACGTAAACGGTGGGCCTGAACTTGACCGTTGCCTGAGC
CCTGAAGGTGTGAATGGAAACGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA
ATAGGGAAGGTCATCGGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCGTGGACAGGTAC
ACTGGAAAAGAGTTTGCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT
CTGATTGAGAACGAAGTGTCAATCCTGCGCCGAGTGAAGCACCCCAACATCATCATGTTG
GTTGAAGAGATGGAAACAGCAACTGACCTCTTTCTAGTGATGGAACGGTCAAAGGTGGA
GATCTCTTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCAGGCCA
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG
GCAGCTGGTGTGATTACATACTTCTCTGTGGATTCCCACCATTCGGGAGTGAGAAC
AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATTCACAGCCCC
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTTAGGAAATGCTTATGAAGCTGG
CCCGTGGGCTTCCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG
TGTCATCTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC
CGCGGGGACGGGGGCATGGTGCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC
TGGCAGTTTTCCCTGTTTTCCACCACCCCACTCTTTTAATAATTGTATATAACTGTACT
TGTTCTACTTGCTTGTCTTTAAACAGGGGGCCCCACAGTTCACCTCTCACTGTTAGATTT
TGCCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

SEQ ID NO: 26_AA383293_H

CCAGCAGCCAAGAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG
CTGGTGGTGA CTCAACGCCGCTTCCCCACCATGGAGGCCTTCCCTCTGCGAGGTGACATCA
GCTGTGCAGGCCCCACTGGCTGTGCGTGCCCTCTACACACCTTGTTCATGGCCACCCTGTG
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

46/113

FIGURE 2S

CACAAGCTCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTTCAGGAATGGGGACCTGGTA
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAACTGTGTTG
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG
GGGCTCCCCTGTGAGCAGGGAAGGAGCTGGTAAGTGGCCATTACTATGTGGCTGTGCGA
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA
GGCAATGAAGCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCCAAGCCTCTT
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG
TCAGAAACAAGCAGAGACGGGCAATCATTCCCATCAGGAGTTATAGGAGTATATGGAGCT
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGGAACAGGTTACTTGTCTGCAA
GACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTTTCGTTATGCC
CAAGATGACTTTGTCTGGATCATAGTCGTGACGGCTCCTGAGAGAGCACCAGGCGGGC
TTTGAGAAGCTCCGCAGGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA
TGTATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG
GAGCCCAAGACGAGGCCAGAAGAGAACAAGCCAGAGCGGCCAGCGGTGCGAAGCCACGG
CCCATGGGCATCATTGCCGCCAATGTGGAAAAGCATTATGAGACTGGCCGGGTGATTGGG
GATGGGAACTTTGCTGTGCTGAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCG
ATGAAGATCATTGACAAGTCCAGACTCAAGGGCAAGGAGGACATGGTGGACAGTGAGATC
TTGATCATCCAGAGCCTCTCTCACCCCAACATCGTGAAATTGCATGAAGTCTACGAAACA
GACATGGAAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTTGACGCCATC
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGGACCTCAAGCCGGAAAAACCTT
TTGGTTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTGGACTTGCA
AAGCATGTGGTGAGACCTATATTTACTGTGTGTGGGACCCCAACTTACGTAGCTCCCGAA
ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGGCTGCTGGCGTGATCCTC
TATATCCTGCTGTGTGGCTTTCCCCCATTCGCGAGCCCTGAXXGAGGGGACCAGGACGAG
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTCCTCCCCCTTACTGGGACAATATC
TCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTGGTGGTAGACCCCAAAAAGCGCTAC
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG
AAACGACAGAAGCAGGTGTCCCCCAGCAGCGATGGTCACTTCCGGAGCCAGCACAAAGAGG
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCCAGTTCTGCTC
AAGGACAGAGAAAAGGATAGAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTCACATA
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAAAAAATTAAGT
CAATGTTAAATGTCACAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATACATTTT
TGGGGGGTAAGCATTGTCATCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC
CTTTGTAACCAAGTTTATTCTGTACTACAGGAGTGGTGCTTACCAGGGTCTAAACTCCCC
CTGTGAGATTAATAAGGTGCATTG

SEQ ID NO: 28_AA197883_M

ATGCCAACCGCGCCGGTCTGCGCCCGCCGCCGCCAGCGACCCCGCCCGCCGGCA
CCCAGTCGCCCTGCGCCTCCCATTCGCGGCCACCGAGGCCCATGTGACCATTCTCTGAAA
TGCTTAAGCTCGAAGATCTCTGAGAGAAAGCTGCCAGGCCCTGGTTACCTGCGGGACGA
GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGCCGTGATGCCGCTGTTACGCCCT
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCCTGAAGCCCAGGGTGGTGACG
GTGGTGAAGCTGGGTGGGCAGCCCCTCCGTAAGGCCACCCTGCTCCTCAACCGGCGCTCA
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG
AAGAACGACCGTGTGCGGAAGCTGTTACCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT
GACTTCTTCCGGGAGGGTGATGCTTTTCATAGCTATGGGCAAAGAGCCGCTGACATTGAAG
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCCCT
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCCAGCAAGCTTCTGAAAGGA

FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAGAAG
TGGGTAAGAGGGAAACAGGAGTCAGAACCTGGTGGCCCGCCTTCACCCGGGGCAGCCACT
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC
GGGGAGATTGTCAGATGTGAGAAGTGTAAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG
AGGGAGCCGTGCCCCGCTGGGAACCAGTGAGCTGGACCTGGGGAGAGCTCAGAAGAGGGAT
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
GGAGAGGAAGGGTGAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA
ATGAGGAGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC
AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA
GAGGAGGGGGCCGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAAGCATGCC
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGAG
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTTCATT
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGACAGTGAG
ATTTTAATCATCCAGAGTCTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTTGATGCC
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCGAGGCTGCAGTTATGATCACAGACTTGTGT
AAGGCCTTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC
CTCCTGGTTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGTCTCT
GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC
CTATACATCCTCTTGTGTGGCTTCCCCCCTTTCCGAAGTCTGAGAGGGACCAAGACGAG
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAAGTTTCTCTCTCTTACTGGGACAACATT
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC
ACGGCCGAACAGGTCTTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG
AACTCACAGAAGGAGGAGTCCCCCAACAGTTTAGGTCACTTCCAGAGTCAGCACAGAAG
GTTGCAGAGCAGATGCCATAA

SEQ ID NO: 29_DRAK2_H

CTCCGCTGCTGTGCCAGGAGTCACTTCACGAGAAGCCAGGTCACAACCGTCGGCCCTTG
TCTGGAAAAGTAAAAGTGGATCCTGCCACGTTTCGGAGCTCCCTGGCGCCTCGCCCGGCTG
GAGCTAGAGAACTCGTCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCCCTGGA
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCCGGAGCGGTAAAAATAAGTGAATAAAGAAG
CAGACCTGGGAATCACCTAACATGTGAGGAGGAGATTTGATTGCCGAAGTATTTAGGC
CTACTAACTACAACCTCCTCAAATTTCAATAAAAAATGGAAAACCTTAATAATTTCTATATA
CTTACATCTAAAGAGCTAGGGAGAGGAAAATTTGCTGTGGTTAGACAATGTATATCAAAA
TCTACTGGCCAAGAATATGCTGCAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT
ATTAATCTTCATGAGGTCTATGAAAATACAAGTGAAATCATTTTGATATTGGAATATGCT
GCAGGTGGAGAAATTTTACGCCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT
GATGTTATCAGACTCATTAACAAATACTTGAAGGAGTTTATTATCTACATCAGAATAAC
ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCCTCTCGGG
GACATTAATAAGTAGATTTTGGAAATGTCTCGAAAAATAGGGCATGCGTGTGAACCTCGG
GAAATCATGGGAACACCAGAAATTTTAGCTCCAGAAATCCTGAACATATGATCCCATTACC
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT
TATTCGGAAGAACTTTTTTCATCAGTTTCACAGCTGGCCACAGACTTTATTTCAGAGCCTT

FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA
CAGCAGTGGGACTTTGAAAACCTTGTTTCACCCTGAAGAACTTCCAGTTCCTCTCAAAC
CAGGATCATTCTGTAAAGTCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC
TGTGGTGATAGAGAAGACAAAGAGAATATCCAGAGGATAGCAGCATGGTTTCCAAAAGA
TTTCGTTTCGATGACTCATTACCCAATCCCCATGAACTTGTTTCAGATTTGCTCTGTTAG
CACTTTTTTCTTTGACTCATTGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA
ATTTAGGGAAGTGTTTAATGTAAATTACTAGTTGCTAGCATGTTATGATTTTCATATCC
TGAGATAGCTCTGCAGATAAGAAAATATTTAAATATATGACAAAAGTAAAATTGTACAT
GTGAAAG

SEQ ID NO: 30_W44160_M DRAK2_M

CCAGACGCGGCTGCACTTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG
GTCGCCGCGGGAGTGCCTCACAGGGGCCTGGCTGACGGCGACCAGCCGTTGTGGGGAA
GAGTGCGAGGTAAAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA
GGAGATTGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCAAAAGAACTTGGGAGAGGAAAAT
TTGCTGTGGTTAGACAATGTATATCAAAATCAACTGGACAAGAGTATGCTGCCAAATCCC
TGAAAAAGAGGAGAAGAGGGCAGGATTGCCGGGCGGAAATTCTGCATGAGATAGCTGTGC
TGAGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC
CTGAGTTAGCCGAAATGGTATCTGAAATGATGTTATCAGACTCATTAACAAATCCTTG
AAGGAGTTCATTATCTACATCAGAATAACATTGTTTACCTTGATTTAAAGCCACAGAATA
TACTTTTGAGCAGTATATACCCACTCGGGGACATAAAAATTGTAGATTTTGAATGTCTC
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC
CAGAAATCCTCAACTATGATCCCATTACCACAGCAACAGATATGTGGAATATTGGCATAA
TAGCGTATATGTTGTTAACTCATACATCACCATTTGTAGGAGAAGATAATCAAGAAACAT
ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTTCATCAGTTTCAC
AGCTGGCCACAGACTTCATCCAGAGCCTTCTAGTAAAGAACCAGAGAAAAGACCAACAG
CAGAATCCTGCCTATCCCCTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTTCATC
CTGAGGAACTTCAGGCTCCTCTCAAATTCAGGATCTGACTCTCAGGTCTCTGAAGAGA
AGACCTCCAAGTCCTCCTGTAATGGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC
CTGAAGATGGCAGCTTAGTTTCTAAAAGATTTTCGATTTCGATGACTCCTTGCCAGCCCC
ATGAACTTGTTCCAGATTTGTTCTGTTAGCATTTTCTCTGTGACTCATCTGGACTGACT
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT
TATAAATGCACTTCTGCTTAGAAGAACTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG
GCTAGCATATCATTTCTTGTCTGAAATTGTTTTGCAGAGGAAAATATTTAAGTATATGA
CAAAAAATGTAAATTGTGTTTAAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA
GACTTATAAAATGGGTTATATTATGGTTAGTAAAAGTTGAAAAAAATGAAAACAGGAAT
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAAATACTCCAGAGAGAGTTTA
TAGTTGAAAGTATTTCCCAGTTACCAATAATAGCTTGAAACTGTAAGATTTTCTTTGTGT
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGGTTGATCCAGGCTGTTTCTC
TGCAAACCGAGTCAAACTCGACATCATTTCCAGCTCATGTATTTTGTACGTGCATCATA
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAATAAGAGGCCTTTGTCTTCTAGA
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTGTTGGATGTCTCCTAAGTCT
CAGGATAGAAGCCCATCATTAGAGCATAGGCACTTCAGGAATTCTTGTGTGAAATTCTAG
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA
CACAACACATGGGAGTGTTCAGTGTGTGTCGGTGGTCAATATCTATGTTTCAGTCTGATGG

43/113

FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCAGTGGTGTCCATTTTAAGGTCTGTAATA
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA
ACAAATTAAGCCCTGTGTATTGAAGTGGGTGTTAGTCTAACACCTGTAAATTCTTGAA
ATTGTTACTAAAATTCCAAATTCCTTAGATAAATTTAACTATTTAAATTGAGCATTGCT
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTTTAAAGGAAAAGTTGT
TTGCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT
GATAGATAAAATACAGCCTTTAAACAACCTTC

SEQ ID NO: 31_H01248_H, DRK1_H

ATGATCCCTTTGGAGAAGCCAGGCAGCGGGCTCCTCCCCAGGCGCCACCTCAGGCTCG
GGCCGGGCAGGCCGGGGTCTGAGCGGGCGCTGCCGGCCGCCGCCGCCGCCAGGCCCGC
GGGCTGCTGACAGAGATACGCGCCGTGGTGCACCGAGCCCTTCCAGGACGGCTACAGC
CTGTGCCCCGGGCCGGGAGCTGGGCAGGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAG
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAAGAAGAAAAGGCCAAGAT
TGTCGGATGGAAATAATTCATGAGATTGCTGTACTTGAAGTAGCACAAGACAATCCTTGG
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT
GCTGCTGGGGGTGAAATCCTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTACACACTCGT
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTG
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCTTAGTTATGATCCTATA
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTTAACATATGTCATGCTTACAGGAATA
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACA
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTCAGGATGGAAAAGGCACTAGAAGAAGCA
AATGCCCTCCAAGAAGGTCATTCTGTGCCTGAAATTAATTCCGATACCGACAAATCAGAA
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA
TGCAGACAGTCTGAAAAAGAGAAAATGGAGCAAAAGGCCATTTCCAAACGATTTAAATTT
GAGGAACCTTTGCTACAAGAAATTCAGGAGAATTTATCTACTGA

SEQ ID NO: 32_AA021445_H

CGGGGCTGCCGGGGCCGGGACTGGGGGAGCCGGGGCCGCCGGCCGCTGCTGCCTCCGCC
CGCGCCGGGGTCCCCAGCCGCCCGCTGCCGTGTCCCTGCGGCCGGCCAGCCGCGTCC
CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCCGTATCGGCTACTACGAGATCGACCG
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT
TTTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCATATCATCAGGCTCTACCA
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTCGGAAGTTCAA
ACAGATCGTCACAGCTGTCTATTTTGTCACTGTCGGAACATTGTTTCATCGTGATTTAA
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAATAGCAGATTTTGGTTTCAG
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCAAAGTGGACATCTGGAGCCTTGG
AGTTGTCCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA
TCTGCGGGCCCGCTGCTGAGTGGAAAGTTCCGCATCCCATTTTTTATGTCCACAGAATG
TGAGCATTTGATCCGCCATATGTTGGTGTAGATCCCAATAAGCGCCTCTCCATGGAGCA
GATCTGCAAGCACAAAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCCT
CTTGGCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

50/113

FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA
AACCTTGCCTCTCGGAGCACTTCCTAGCATGCCCCGAGCCCTGGCCTTTCAGCACCAGT
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT
GATCAACCCAGAGAACCAAATTGTGGAGCCGATGGGACACTGAATTTGGACAGTGATGA
GGGTGAAGAGCCTTCCCCTGAAGCATTGGTGCGCTATTTGTCAATGAGGAGGCACACAGT
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT
TCCTGGAGTCAACCCCCAGGCTCCATTCTGCAGGTGGCCCCCTAATGTGAACTTCATGCA
CAACCTGTTGCCTATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC
TCTCCTACAGCCGCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC
ATCAGATGGAGGAGCCAACATCCAAGTGCATGCCAGCAGCTGCTGAAGCGCCACCGGG
ACCTCTCCGCTTGTCAACATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA
GAGCTCAGACGGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA
AAGACATACACTGGCCATGACCAACCTACAGCTGAGATCCCACCGGACCTACAACGGCA
GCTAGGACAGCAGCCTTTCCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAT
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA
CGGGGGGAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCTCTCTCA
GCCATCTCCACCTCTTACAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT
CCAGAGGTTAAGGATTACAGCCTTCAAGCCCACCCCCCAACCACCCCAACAACCATCTCTT
CAGGCAGCCAGTAATAGTCTTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC
TGCACTCTTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC
TGAGAACTGTTCTCTCTCTCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC
TCAGTCACAGCAGGTCAACATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT
GCAGATGCAGCACCGTACCAACCTGATGGCCACCCTCAGCTATGGGCACCGTCCCTTGTC
CAAGCAGCTGAGTGCTGACAGTGCAGAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTCGGACCAGTCCCGGGGTTC
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTCTCTCCAACCCAAGCCCTGAAAGT
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGCACATCAGCAGCCGCCACACTA
TACCACGTGCGCACTACAGCAGGCCCTGCTGTCTCCCACGCCGCCAGACTATACAAGACA
CCAGCAGGTACCCACATCCTTCAAGGACTGCTTTCTCCCCGGCATTCTGCTACCGGCCA
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGACACAGCTCATTTAAAGGCAGCAGCAACA
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAAGTGTTCAGGCACAT
GAACCAAGGGGATGCGGGGAGTCTGGCTCCCAGCCTTGGGGGACAGAGCATGACAGAGCG
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT
GCTACAAATCAGGGCACAAGAATGTGTCTCACAGGCTTCTTACCCACCCCGCCCCACGG
GTATGCTCACACAGCCGGCACTGATGCATTACAGAGAGCATGGAGGAGGACTGCTCGTGTGA
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAAGGTTGCCA
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCCTGAATCTTTGCTAGGAAC
TGTGAGTCATGCCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAAGTGTGCATT
CAGTAAAAATAAGGTGCCCAGCAGAGAGCCTGTATAGGGAACTGCATGGATAGAAGTTC
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCTC
CGTCCATGAGCACACAGGCCCCCGGGCCCTCCAGAGACACCACACGATCCAGAACAGCGA
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT
TAGCTCTGCCCGGATGTCGGATGCAGTTCTCAGTCAGTCTTTCGCTCATGGGCAGCCAGCA
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTCATGAGCACCAGCA
CCTGAGTGATGGCAGCCAGCATTTAACTCCTCTTGCTATCCATCTACGTGTATTACAGA
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTACAGCATGGAGCAGGCAGGCGTGTA

FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGAATGAAAAGGTTGATTGTAAACCCACA
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC
TGCTTTTCCTCACATTTGGTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC
CATGTTTGCTTGATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC
C

SEQ ID NO: 33_2R22-5-11_H

CTGGGCGGCTGCCGGTCAGGTCGGCCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG
AACCAGCCAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTTCATCTAAATAAAGGCC
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT
TATTTGCAAGTTTCTTCTTTCTTGGGGTCCAGATTATTAGGTCTCCAGCGCCCTGCAGCT
TGACAGAAAGAGAAGCATGAAATGAAGGTCAGAGATGAGATCCCGCAGCAGGGACGTGGG
GGCCTCCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG
CAAACAGAAGCCTTTGTCTTGGGGCACAGCCACCTACCACAAAGCATCAGACTCCACGTC
TGGCCAGAAAGTTCTTGGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCTCTACTAAA
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACCTCTTTGAACCCTGGGCACCTGCTGT
CCTCAGTTGGCATCTCCACCCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG
CTGAGATGGAGACGTGAGCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTGAG
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA
CTGACACAGGACATGTCCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG
ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAAACTTCTCCCAAGTGAAGCTT
GGGATTCACTCCCTAACCAGAAAGAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA
GACCAGAAAACCCAGAGGCTACTATCCCGAGAAATCTCCAGCATGGAAAAGCTGCACCAT
CCCAACATCATCCGCCTTACGAAGTGGTGGAGACCCTATCCAAGCTGCACTTGGTGATG
GAGTATGCAGGGGGTGGGGAGCTCTTCGGAAAAATTAGCACTGAGGGGAAGCTCTCTGAA
CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC
CAAATTATTATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG
AAGGTGGGCGATTTTGGATTGAGCACAGTAAGCAAAAAGGTGAAATGCTGAACACTTTC
TGTGGGTCTCCTCCCTACGCTGCGCTGAACTCTTCCGGGACGAGCACTACATCGGCATT
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGACTGGCACCATGCCA
TTTCGGGCAGAAACCGTGGCCAAACTAAAAAAGAGCATCCTCGAGGGGCACATACAGTGTA
CCGCCGCACGTGTCAGAGCCCTGCCACCGACTCATCCGAGGAGTCCTTCAGCAGATCCCC
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC
CCTACACCTTTGGAACCTTTCCAACCTGGATCCCAACATTTGTCTCGGAAACCAGCACTCTC
AAGGAAGAAGAAAATGAGGTCAAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT
ATTGCAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCCAGTCATGATGCTACCAGAC
CCTAAAGAAAGAGACCTCAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC
AAATTTTGTCTGATTTTATAAATTGCACTAGACTGCTTGTAACTAACCAAGATGATTGTT
GCTGCTTCTAAATTTTTTTCAAGGACAACCTTGAGTGGAGACATTTTTGTAAATTTTAAAT
AAACTTAAATTTGAGATATGCAAAAAA

SEQ ID NO: 34_R31237_1_H, AAC33487

ATGTCCACTAGGACCCCATTTGCCAACGGTGAATGAACGAGACACTGAAAACCAACACGTCA
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAACTACAGACTGTTGAAA
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAAATTGGCAAGACATATCCTTACAGGCAGA
GAGGTTGCAATAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTTCGAA
GTCATTGAAACTGAAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA
TTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAAATAGCAGATTTTCGGTTTTAGC
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAGTCTCCATACGCAGCA
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAAGTGGATGTGTGGAGTCTGGGG
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCCTTCTACATGTCTACAGACTGT
GAAAACCTTCTCAAACGTTTCTTGGTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTTGTT
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA
TATTTGTTATTGGGGAGAAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT
CCTCACCACAAAGTGCAGAGAAGTGTTTCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC
CATGCTGGACCAGCTATTCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTCCCGGAAATCAAGTGGCAGTGCTGTT
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG
GCGGATATTCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT
GGAATGACACGACGAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA
GTGATTTCAGAAATGGCAAAGAAAACAGCACTATTCTTGATCAGAGAACTCCAGTTGCTTCA
ACACACAGTATCAGTAGTGCAGCCACCCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC
AGTCGTAGCACTTTCCACGGCCAGCCCCGGGAACGGCGAACCAGCAACATATAATGGCCCT
CCTGCCTCTCCCAGCCTGTCCCATGAAGCCACACCATTGTCCAGACTCGAAGCCGAGGC
TCCACTAATCTCTTTAGTAAATTAACCTCAAACCTCACAAGGAGTCGCAATGTATCTGCT
GAGCAAAAAGATGAAAACAAAGAAGCAAAGCCTCGATCCCTACGCTTCACCTGGAGCATG
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAAGTGTTGGAC
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT
GGGCACGCGGAGAACCTCGTGCAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT
CTGAACGGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

SEQ ID NO: 35_W90839_M

AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCGTTGCCGGAACCTCTATCGCTTCC
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCGGGAGGTCGCTATTAAG
ATCATTGATAAGACCCAGCTGAACCCCAAGTAGCTTGCAAGAGCTGTTTCAGAGAAGTCCGA
ATTATGAAGGACTCAACCACCCCAACATCGTGAAGCTTTTTGAGGTGATAGAGACGGAG
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTGTTGACTACCTCGTG
TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTCAGCC
GTGCACTACTGTCATCAGAAGAACATTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCGGCTTCAGCAATGAGTTCACGCTG
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATACGCCGCCCCAGAGCTGTTCCAG
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCTATCCTGTACACG
CTGGTCAGCGGCTCCCTGCCCCCTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC
CTCAGAGGAAAGTACCGGGTCCCCTTCTACATGTCTACAGACTGCGAGAGCATTTCTGCGG

FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG
CGGATGCCGGGTTCGGAAAGCGAGCTGCAGTGCAGTGGGCAGTGGAAAGTCGAGGCTTGCCC
CCCTCCAGCCCCATGGTCAGCAGTGCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG
CGGAAGGACAGCACTAGCACCCCTAACAACTCCCCCAGCATGATGACCCGAAGAAAC
ACCTATGTGTGCACAGAGCGACAGGATCTGAACGCCCGTCTTGTGGCCAAATGGCAA
GAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCCTGGCT
CCCCCGTCAGGCGAGCGGAGCCGCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA
CCCCCAGCCTCACCCACGCTTGCCACGAGGCCGCACCCCTGCCCTCCGGGCGGCCTCGC
CCCACCACCAACCTCTTCACCAAGCTGACCTCCAACTGACCCGAAGGGTCACAGACGAA
CCTGAGAGAATCGGGGACCTGAGGTCAAGTTGCCATCTACCTTGGGATAAAACGGAA
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

SEQ ID NO: 36_406786.5_H

GTAGCCGGCTTGGCGTGACCGTCCGCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT
GGCCTCCCTTCTTCCCATGGAGGTGGGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG
CCTTTCCAGAGCCTCCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC
TGAGCCCAGCAGGTGCTTTCTCTCAGCCCACAGACACCTGAGCAGAAGGAATGGGCTTTC
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC
ATCACTGGCTGCCCAGAATATTTGTACAAGTAACTGCACTGCCCTGCTGCCCCCTGAGCA
CACGGACCCGTCCGAACCGCGGGGCAGTGTGTCTGCTGCTCCCTGCTGCGGGGACTGTC
CTCAGGGTGGTCTTACCTCTGCTTCCGGCCCCCTGTGTGCAACCCTAACAAAGGCCATCTT
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGGCGGGCTCCT
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTCTTTCTGAGGTGAGA
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT
GGTGTGTTTGGCACGGTGGTGGACATCATACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCTATGCTGCGTGGTGGTCTTGGAGCCCGT
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTGATGTGACAG
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA
GATTGAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGGCCCCCTGTGAGCGGCTA
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCTCCTGCCGGATGG
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAGACGGA
GCTCCTGGGCAAGAATATCACTTTCTGATTCTGTTTCTACAGCTACATGGACCTTGC
GTACAACAGCTCATTACAGCTCCCAGACCTGGCCAGCTGCCTGGACGTGCGCAATGAGAG
TGGGTGTGGGGAGAGAACTTGGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA
GGATCCAAGGATTAATGTGCTGCTTGCTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG
GAAGCTGATGGAAAGCCAAGACATCTTACCCGGGACTCAGACTGAGCTGATTGCTGGAGG
CCAGCTCCTTCTGCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCCAGAAGG
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCCTTGGG
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC
TGAACAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC
TGAGGATGGGGCAGTGTGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG
GATGGGAGTCAGTGGTCCCAGCGGTTACAGACCTTTGGGCTGGGGCTGCCGTGGCCAAGCC
CCAGGCCAAGGGTCAGCTGGCGGGGGCAGCCTCCTGATGCACTGCCCTTGCTATGGGAG
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCCTCTGGGATGGCAGG
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAACGACCCGAGA

FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGACGAGCCCT
GGATGTCCCCACGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG
CTATGCCTTGCCACGGACCTCCCTGGGGGCTTGGAAAGCAGTGGAGGCCCAGGAGGTTGA
TGTGAATTCGTTTTCTGGAACCTCAAGGAACCTTTTTTCAGTGACCAGACAGACCAAAC
GTCATCAAATTGTTCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCCTTGGCAGT
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCTGTGTCTTGGATGACAG
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCCGGGA
GAGCTGTGTGGGACATGATCCAACAGAACCCTTGAGGTTTGTGTTGGTGTCTCTGAGCA
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCCCTTCCACGTTGGATGCTGGCCC
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTCACCTCCACGCC
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGGTGCCTACTC
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAAGACCTCCTCCACAG
CCAACGCGACTCAGCCGCCAGGACCCGCTGTTCCTTGCCAGCCTGCCCGGCTCCACCCA
CTCTACCGCTGCTGAGCTCACCGGACCCAGCCTGGTGGAAGTGCTCAGAGCCAGACCCTG
GTTTGAGGAGCCCCCAAGGCTGTGGAACCTGGAGGGGTGGCGGCCTGTGAGGGCGAGTA
CTCCCAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC
TGCTGTGGACAAGGGAAAAACAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT
CTTGAGGATTGTTGGATTGAGGATCCCAAACCTGGGAAAGTTACTTTAGAGATCGCAAT
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA
CCGCCACCCAGGCTGGATGAGCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG
CCAGAGCCGTCTAGTGTACGAGTGGGATACCTGCGCTTGAAGGACATCATCCACCGTGA
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG
CTCGGCCCGCTACTTGGAAAGGGGAAAATTATTTTATACCTTTTGTGGGACCATCGAGTA
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCCTTCTGTGAGCTGGAGGA
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCCAAAGAACTCATGAGCCTTGT
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA
CCCGTGGGTAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT
GAGTGATGTGGCCCAGGCTCAGGAGCTTTGTGGGGGCCCCGTTCCAGGCGAGGCTCCTAA
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCCGTCTGCTGACCAGCTAAACACCAATTTT
TTCCTGCTTTTCTCCACTTGGTTTGGAAAATCACACAGTTTTTCAGGCTCCATCTGTTTG

SEQ ID NO: 37_AA544838_M 406786_M

CCACGCGTCCGCATCCCTGCTTGATGAGCCCTGGCGAGTTTCATCTTTCGACAACCTAG
TGTCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA
ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT
TAGAGAGGGGCAAACTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTACCCC
TGTAACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG
TTATTCATCCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC
AGCCTTGCCCTGAGCAGCGGACCACTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA
GTGGCCTGCTGTGACGTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCCAGGGAGACTCGTGGTGACCAGCACTGCT
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG
GGCAGTTGTATGGATTTTACAGGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

53/113

FIGURE 2BB

TGACTTCTGCTTCTAGATTCCCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTTATAACCTTGAAAATCATTCTAATG
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG
TGTTTAAGTTCTCTATTTTTTGTGTTGTTGTTTTTGCTTGTAAGTTTTTGAGACAGGATCTC
ACCATGTAACCTTTGGCTGGCCTGGAACCTCACTATGTAGACCAGGTAGACCTTAACTGA
CAGATCTGCCTGCGCTTGCCTCCCAAGCATTAGGACTGATGGTGTGTGTCAACCATGCCCA
GTTCTTCCTGGTTTTTGTGTGTAGGTTTCTTTCCCACTGACTTGGTACATGTGACATGTGA
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAAATGGCCAGAATATTTATTTATTTT
CTTAAAAATTTTCCAAATTAAAGCTACTTAGTTAACAGTTAACTGGCCAGGACTATATG
AGATAAACTTGGTTTTCTATTTCTTTTTGT

SEQ ID NO: 38_AA785735_H

GGCACGAGGCGCGCCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA
GCAAGCGGAGCGCAGTTCGCCCAAGCCAAGCCGCGCTGCCAACCCTCCCGCCCGCCCGCG
CTCCTGTCCGCGGTGTCTAGCAGCGGGGCCAGCATGGTCATGGCGGATGGCCCGAGGCA
CTTGACGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACCTTATCAGGTAATGGAGACCAA
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAATTTTTGACTATCTTGC
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTTCTGGCAAATCCTGTCTGC
TGTTGATTATTGTTCATGGTCCGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT
GCTGGATAACAACATGAATATCAAAATAGCAGATTTCTGGTTTTTGAAATTTCTTTAAAG
TGGTGAACCTGCTGGCAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT
TCTGGAAGGAAGATTCCGGATTCCGTATTTTCATGTCAGAAGATTGCGAGCACCTTATCCG
AAGGATGTTGGTCCTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA
ATGGATGCTCATAGAAGTTCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA
TGAGCCATCCATCGGGGAGTTAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAT
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAGAGCTATAACCACTTTGCTGCCAT
TTATTTCTTGTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGGAGCAGAG
ACTTGATGGCCGCCAGCGTCGGCCTAGCACCATTGCTGAGCAAACAGTTGCCAAGGCACA
GACTGTGGGGCTCCAGTGACCATGCATTCACCGAACATGAGGCTGCTGCGATCTGCCCT
CCTCCCCCAGGCATCCAACGTGGAGGCCCTTTTCATTTCCAGCATCTGGCTGTGAGCGGA
AGCTGCATTTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA
CCCTGTGCCTCCTGTCTGGTGGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCGGAGGAAGACCCCGCTCATGC
CTTTGAGGCATTTTCAGTCCACACGACGCGGCAGAGACGGCACACTCTGTGAGAAGTGAC
CAATCAACTGGTCGTGATGCCTGGGGCAGGGAAAAATTTCTCCATGAATGACAGCCCTC
CCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTTCAGAGGGACCTGAACTTTCT
GGAAGACAACCCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCCAGAA
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGAGAGCATCAGATAC
CTCCCTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAGAACCAA
AGGAATTCTAGAGTTGAACAAAGTGACAGTTGTTGTATGAACAAATAGGACCCGAGGCAGA
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCAGCCT
TCTGTCAAAGGCCCAGAACACCTGTCAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA
ACTGCAGGCCTATTTTAAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA
GCAGCTGCCCCCTTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTTCAG
CCTGACCCAGCCCCCTGAGCCCCGTCTGGAGCCTTCTCCGAGCAGATGCAATACAGCCC
TTTCTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCCTGCCCTCCACTTCCGGTCCCCG
GGCTGCTCCTCCTCTGCCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG
TGAGCTGCCAAGCGCTGCTTCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCAGAAGCCCAGGACTGCA
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCCTGGTGAATTAGTCTCA
GCACAGGAATTGAGGTGGGTGAGGTGAAGGAAGAGTGTATGTTCCCTATTTTATTTCCAGC
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCCCTCGTTCTGCCCCACCA
CAAAGTTTTCTGTGGCAAGTGCTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG
AACCCGGGAGGCGGAGCTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCG
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC
TGTTTTCTAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGGCAG
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA
TTTTTGTCTTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC
ACTGGGGCACAGATAGAGAACCAGGCGGCAGCAGTGCTCGCAGACCCACCCAGGGAGAGC
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT
TTGTACATTAGTTTTTACCAAGCACTTTCTCTTCTAACCCCTCACAACAATTCTATGAAATT
AGCTGGGGAGATACTGTCTTATTTTTTCACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTTGAC
TGGCTTCTGGTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTTCCCTTCT
CTTTCCTCAGTAGCATCTGACTCTTTTTCATAAGCAAACAGCTGTATAAACAAGCCCCCA
TTTTTGGTCAAGCACAGGGTGAATGTGATATTGTTCCCACAACCTTATTCTCCACTCAACA
GCCGCTGGCTTTGGGGAAGAGGCCGCTTTCAGGTGACAGTGACAGCTGTCCAGGTGGCCG
TGCACTGAACCAGGCTGAGGGAGACAAAAACCCCGCAGACCCGCTGCCTTTCAGCGTCC
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC
AGCAGTTTCTACAGAACACCCCCCTTCTCAATTGCCAAGGGGCCGCATCGCACGGCATC
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCATGAACTCAGCCTTTGT
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGCCCCATCAACTAGAAGTGCTTATTA
CTTTTAGGATTAAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTTCAGAGGCA
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT
ATGACCCAGATGGAATAATGTCACATTCCCAGTGACAGATAATGGGCTGCTGCTGGCTC
TGTGGTGTCTGTCTGCAGAAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC
CACCATGGGTGGTAAGAGAAACCTGCCTTACCAAAATCTCTGAAGGGGAAAGAAGTGGA
GAGAAAGGTTTGTCTTCACTTCGGGGACTGCAGTTTGAGAAATAAAAGGGATACAGAGATA
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT
TTTCTGTGTGCTTTTTTTTAAATTAATAAGAAAAAAATTTGGTGAGTTCAGTAGCTTTGGTA
TTATGAGTGCAAATCATAATAGCTCCAATGTGAAAAAAATCAAAAGTATAAATTGTC
ACTTAATGTTAGAAAATTGCCTAAAATGCAGTGTAATAAATAATCTCTGTACCAAATAGT
AATTTAAATGGGGTAATTTTCTGCAAGGAAATGTACTGTTTTTATGTTTTCCAACCCTCT
TGA

57/113

FIGURE 2DD

SEQ ID NO: 39_AA207220_H

GCTGTGGCTCCCCGTCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTTC
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGAGAGCTAGCCCCGGCCGCTGGCGGAAGGG
CTGATCAAGTCGCCCAAGCCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG
CACAACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGGAAG
GTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCA
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTG
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC
TACCGGGAGCCACCTAAACCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG
GTGAACCCACCCGCGGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT
GACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGCGTTCCTCCCGCCCCCTCCTGGAG
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC
CCTGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCAG
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGAC
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCCAGGGCAGGCTGCCCCCTGCTCCCCAAG
AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCC
AGTGAATCTGGGGAGCTCTTGGACGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT
GGCAAGTTCTCCAGACAGCCTTGGAGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT
GAACTCGCCCCACCTCGCCCCCTGGCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG
GACAGCATCCTGTCTCTGAGTCTTTGACCAGCTGGACTTGCTGAACGGCTCCAGAG
CCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCTCA
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTT
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCCGGTGAGGCTCTCAGATGCAGCTGG
TTGCACCCCCGAGGGGAGATGCCTTCTCCCCACCTCCAGGACCTGCATCCAGCTCAGA
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG
AAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA
GAGGGGAACGGGAATGCCCCGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG
GGCCACAGAGA

SEQ ID NO: 40_AA426580_H, MAK_V_H

ATGCCGGCGGCGGCGGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCCTGGGGGCGGCGGC
GGCGCGGAGGACGCGGCCAGGCCCCGCGGCGGCCTGCGAGGGAAGTTTCCTGCCTGCCTGG
GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCAGCACCACAAGCGCGTGGGCAAC
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG
GACACCTATGTACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC
CCCAATATCACTCAGCTCCTTGATATTTTAGAAACGGAAAACAGCTACTACCTGGTCATG
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

FIGURE 2EE

TCCGAAGCCCCGAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC
GGGGTGGTCCACAGAGACTTGAAGATAGAGAAATTTGCTACTAGATGAAGACAATAATATC
AAGCTGATTGACTTTTGGTTTGGAGCAACTGCGCAGGGATCCTGGGTTACTCGGATCCGTTT
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG
CTGCCTTTTACGGTGGAGCCTTTTCAAGCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA
GAAATGAACCCCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTGCGCTCTCTC
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTCAGCAGGCACTGGCGAATCGCTGGCTT
AATGAGAATTACACGGGCAAAGTGCCCTGTAATGTCACCTATCCCAACAGGATTTCTCTG
GAAGATCTGAGCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC
GACGTGATCAACACTGTGCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTCCTC
TTAAACAAGAACTGGAGCGCTATTTGTGTCAGGGAAATCTGACATCCAGGACAGCCTCTGC
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCTATGAGGCC
TCTCTGGACACCTGGACACGAGATCTTGAATTCCATGCCGTGCAGGATAAAAAGCCCCAA
GAACAAGAAAAAGAGGGGATTTTCTTCATCGACCATTTCTCCAAGAAGTTGGACAAGAAC
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTCAGAACACCAAAGCC
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCTTTGGCTGC
CGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTTCATGGAGTTC
ATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA
GGCCCCGGAAGCACTGGCATCCCCCACAAGGAAGACCCCTGATGCTGGACATGGTGCGC
TCCTTCGAGTCTGTGGATCGCGACGACCAGTAGAAGTGCTGTCTCCCTCTCATCACTAC
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCAGCGAGAGGACGCTGTCC
CCGGGTCTGCCATCCGGAAGCATGTGCGCTCTCCATACTCCTTTGCATCCAACCTCTGGTC
TCTTTTGTCTACGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT
CCGGTTCCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCCACTGCAGCCCCTAGCCCCTGTG
AACCTTGCTTTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

SEQ ID NO: 41_Z36720_H

ATGGACACAAAGCTGAACATGCTGAACGAGAAGGTGGACCAGCTCCTGCACTTCCAAGAA
GATGTCACAGAGAAGTTGCAGAGCATGTGCCGAGACATGGGCCACCTGGAGCGGGGCCTG
CACAGGCTGGAGGCCTCCCGGGCACCAGGGCCCGGGCGGGGCTGATGGGGTTCCCCACATT
GACACCCAGGCTGGGTGGCCCGAGGTCTTGAGCTGGTGAGGGCCATGCAGCAGGATGCG
GCCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAGGATGGTGGCTGCGGTGGACAGGGCC
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTTCATGCAGGGG
CGTGTGCCCTGGAGGAGAGGCAGCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG
AAGGATAAGGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG
ATCATGGTGACAGCGGCAAATAAAGAGCGAGTGGAAGAAGAGGGAGGAAAACCAAAGCAT
GTGCTGAGCACCAGTGGGGTGCACTGTATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA
GCTGACCCCGCCAGGCACTGGTCTCACCGGGCCAGGGAGATGGTGTTCCTGGCCAGCC
CAGGCATTCCCTGGCCACCTGCCCCCTGCCACAAAGGTGGAAGCCAAGGCTCCTGAGACA
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG
GTCTCCCCGAGCCTGGAGGTTGCACCAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT
GACCCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA
GGGCCTCCAGGGCTGCCAGCCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGT
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGCGAGCCTTGGACCCACCCCTCACCACAGAGGCTCCA
GCAGCTGCCCAGCCAGGCAAGCAGGGCCCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCCT
GGGACTGAGCCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCCGCTGCAGGAG
AGCAGCAGCCCCGGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG
CAGCAGGGGCAAAAGCCCAGGGGCGGGAAACCTGAGCCTGAGCAGGACTGTGCAGCCAGG
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCAGGCGCCGAGGCTGGCAGCGTG
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTTCGG
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCCTGAGTGCCTGAGGAGT
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCTTCGAGAGCAAGCACAGCTGC
ACCTTTGTCTATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG
TACCACCTGACTGAGCTGGATGTGGTCTGTTCACCAGGCAGATCTGTGAGGGTGTGCAT
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT
CGAGAGAAGCTGAAGGTGAACCTTCGGCACTCCTGAGTTCTTGGCCCCAGAAGTCGTCAAT
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTCATTGTA
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC
TTTGTTTCCCGGTGCTGGTCAAAGAGAAGAGCTGCAGAAATGAGTGCCACACAGTGCCTG
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAA
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACCTTCTCCCTAA

SEQ ID NO: 42_SGK088_H

GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCCACTGACGTGGAGGTGGATTGG
CTGTGCCGTGGCCGCCTGCTGCAGCCTGCACTGCTCAAATGCAAGATGCATTTTCGATGGC
CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGGCCGGCTGACCGTGCGGCCCTCG
TTGGCACCCCTGTTTACACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC
TGCCCCATGGAGGAGAGTGAGAACTTGCGGCTGCGGCAGGACGGGGGTCTGCACTCACTG
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTGAGTGTGTTAACACC
CATGGCCAGGCCCACTGCTCAGCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCCTCA
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGGTGAG
CTGGAGCGGCTGTCCATTCCCGACTTCCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCACCATCAGCTGG
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT
GTCCATCGCTTGGTGTTCCTGCCGTGGGGCCTCAGCACGCCGGTGTCTACAAGAGCGTC
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCACCTGTATGTACAGATGTGGTC
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGAATCCCTGACGTACACA
GTGCAGCACCAGGTGCTGGGCTCGGACCAGTGGACGGCACTGGTCAACAGGCCTGCGGGAG
CCAGGGTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCTCAGC
ACCACTGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGGAG
CACGGCCCAACCTTGGAGGAGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG
GTGGAGGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGGCCAGGTGCTC
TGGAGGAGCTGCCGAGGGGCCCTCCTAGAGGCACGGGCCGGTGTGTACGAGCTGAGCCAG
CCAGATGATGACCAGTACTGTCTTCGGATCTGCCGGGTGAGCCGCCGGGACATGGGGGCC

62/113

FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTCAACGGCACACAGACCTGCTCGGTACACATTGGAGCTG
GCAGAGGCCCTCGGTTTGAGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAAACT
GCTCGCTTTGCGGTGGTGGTTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC
CTGGTGGTGCTCAGCACGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCCAGAAC
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTCAGCTCAGACAGCTATG
GAGGTGAGGGGGTTCGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCTACTTGCGGGCGCATAGTGGAGCGT
AGCTCCGGCCTGGAGTTTGCGGCCAAGTTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA
GCGCGTCGGGAGGCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT
GAGGCCCTTCGAGAGGCGCGGGGACTGGTCAATTGTCACCGAGCTCTGCACAGAGGAGCTG
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCCTATATGCGG
CAGGTGCTAGAGGGAATACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG
CCTGAGAACCTGCTGGTGTGGGATGGTGTGTCGGGCGAGCAGCAGGTGCGGATCTGTGAC
TTTGGGAATGCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT
GAGTTTGTAGCACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG
CCTGTGGGTGTTGTTGCCCTTCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAAT
GACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCACATTC
CTGAGCCTGAGCAGGGAGGCCCGGGGCTTCTCATCAAAGTGTGGTGCAGGACCGGCTG
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTTCAAACTCAGGCAAAGGGCGCA
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCCCGCGGAGGTGGCAGCGCTCCAG
ATCAGCTACAAATGCCACCTGGTGTGTCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCCA
GAGCGGGTGTGGGTGACCATGCCCAGAAGGCCACCCCCCAGTGGGGGGCTCTCATCTCC
TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCACTGCAGCCC
GAGTTCTCTGGCTCCCGGGTGTCCCTCACAGACATTCCCCTGAGGATGAGGCCCTGGGG
ACCCAGAGACTGGGGCTGCCACCCCCATGGACTGGCAGGAGCAGGGAAGGGCTCCCTCT
CAGGACCAGGAGGCTCCAGCCCAGAGGCCCTCCCTCCCCAGGCCAGGAGCCCCGAGCT
GGGGCTAGCCCCAGGCGGGGAGAGCTCCGAGGGGCGAGCTCGGCTGAGAGCGCCCTGCC
CGGGCCGGGCGCGGGAGCTGGGCGGGGCTGCACAAGGCGGCGTCTGTGGAGCTGCCG
CAGCGCCGGAGCCCCGGCCGGGAGCCACCCGCTGGCCCGGGGAGGCCTGGGTGAGGGC
GAGTATGCCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGAGGCCCCGAGGAT
GGCAAGGTGAGCGGCCTCAGGGGTCCCTGCTGGAGAGCCTGGGGGGCGCTGCTCGGGAC
CCCCGGATGGCACGAGCTGCCCTCAGCGAGGCGAGCGCCCCACCACAGCCCCCACTCGAG
AACCAGGGCCTGAAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG
CACCGCCGAGCGGGGGCGCCCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCGTAGGCTA
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCAGCCATCCAGCCCTGCACGGCCC
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT
GCTCCGAGCCCCCGCACCCAGCCTGCCCAAGACAAGGCTCCAGAGCCCAGGCCAGAA
CCAGTCCGAGCCTCCAAGCCTGCACCACCCCCCAGGCCCTGCAAACCTAGCGCTGCC
CTCACACCCTATGCTCAGATCATTCAGTCCCTCCAGCTGTCAGGCCACGCCCAGGGCCCC
TCGCAGGGCCCTGCCGCGCCGCTTCAGAGCCCCAAGCCCCACGCTGCTGTCTTTGCCAGG
GTGGCCTCCCCACCTCCGGGAGCCCCGAGAAGCGCGTGCCTCAGCCGGGGGTCCCCCG
GTGCTAGCCGAGAAAGCCCGAGTTCCACGGTGCCCCCAGGCCAGGCAGCAGTCTCAGT
AGCAGCATCGAAAACCTTGGAGTCGGAGGCCGTGTTTCGAGGCCAAGTTCAAGCGCAGCCGC
GAGTCGCCCCCTGTCGCTGGGGCTGCGGCTGCTGAGCCGTTTCGCGCTCGGAGGAGCGCGGC
CCCTTCCGTGGGGCCGAGGAGGAGGATGGCATATAACGGGCCAGCCCGGGCGGGGACCCCG
CTGGAGCTGGTGCAGCGGCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTGCGA
GAGCCTGGCCTCGTCCGCGCCCTCTCGCTGTCACTGTCCCAGCGGCTGCGGCGGACCCCT
CCCGCGCAGCGCCACCCGGCCTGGGAGGCCCGCGGCGGGGACGGAGAGAGCTCGGAGGGC
GGGAGCTCGGCGCGGGGCTCCCCGGTGTGCGCATGCGCAGGCGGCTGAGCTTACCCTG

61/119

FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCG
GGCCGCAGCACGCCGCTGTTCCGACGGCTTCGCAGGGCCACGTCCGAGGGCGAGAGTCTG
CGGCGCCTTGCCCTTCCGCACAACCAGTTGGCCGCCAGGCCGGCGCCACCACGCCTTCC
GCCGAGTCCCTGGGCTCCGAGGGCCAGCGCCACGTCCGGGCTCCTCAGCCCCAGGGGAAAGC
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTATCGCCACCA
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTCAACAGTACGTGCGCAGTGAGTCAGAC
TTCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGGAGGCAGCC
ACCCTGCTCTGCCTGCCAGCGGCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG
AAGTCTTGAGGTCAGAGCCCTCAGTGATCATCGTGTCTTGCAAAGATGGGCGGCAGCTG
CTCAGCATCCCCGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCGAGTCCCAGGAAAGCTA
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGCTGTGGAAGCCGGGA
GACAGCCGGGCACCTTGACGTATACGCTGGAGCGGCGAGTGGATGGGGAGTCTGTGTGG
CACCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCGTGCTGGGCAGGGGGCCCTTCAGCAAC
TCTTCTGAGAAGGTCTTTGTGAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGCTGCC
CACCAAGAGGGCCCTGTACCTCAAGGCCAGCCAGGGCCCGGCCTCCTGACTCTCCTACC
TCACTGGCCCCACCCCTAGCTCCTGCTGCCCCACACCCCGTCAGTCACTGTGAGCCCC
TCATCTCCCCCACAACCTCCTAGCCAGGCCTTGTCCTCGCTCAAGGCTGTGGGTCCACCA
CCCCAAACCCCTCCACGAAGACACAGGGGCCTGCAGGCTGCCCGGCCAGCGGAGCCACC
CTACCCAGTACCCACGTACCCCAAGTGAGCCCAAGCCTTTTCGTCTTGACACTGGGACC
CCGATCCCGAGCCTCCACTCCTCAAGGGGTAAACCAGTGTCTTCTCTACTCCTGTGTAT
GTGGTGACTTCCTTTGTGTCTGCACCACCAGCCCCTGAGCCCCAGCCCCCTGAGCCCCCT
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCGGCCAAGGAGGTGGTCAGCTCC
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCTGAGGGTACCACTCTTCGACAGGGTCCC
CCTCAGAAACCCTACACCTTCTGAGGAGAAAGCCAGGGGCGCCTTTGGTGTTGTGCGA
GCGTGCCGGGAGAATGCCACGGGGCGAACGTTCTGGGCCAAGATCGTGCCCTATGCTGCC
GAGGGCAAGCCGCGGGTCTGTCAGGAGTACGAGGTGCTGCGGACCCTGCACCACGAGCGG
ATCATGTCCCTGCACGAGGCCTACATCACCCCTCGGTACCTCGTGCTCATTGCTGAGAGC
TGTGGCAACCGGGAACCTCCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC
GTGGCCACTTACATGGTGTCAGCTGCTACAAGGCCTGGACTACCTCCACGGCCACCACGTG
CTCCACCTAGACATCAAGCCAGACAACCTGCTGCTGGCCCCCTGACAATGCCCTCAAGATT
GTGGACTTTGGCAGTGCCCAGCCCTACAACCCCCAGGCCCTTAGGCCCTTTGGCCACCGC
ACGGGCACGCTGGAGTTTCATGGCTCCGGAGATGGTGAAGGGAGAACCATCGGCTCTGCC
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTT
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCCGCTTTGATGCCTTC
CAGCTGTACCCCAATACATCCCAGAGCGCCACCCTCTTCTTGCGAAAGGTTCTCTCTGTA
CATCCCTGGAGCCGGCCCTCCCTGCAGGACTGCCTGGCCCCACCCATGGTTGCAGGACGCC
TACCTGATGAAGCTGCGCCGCCAGACGCTCACCTTCAACCACCAACCGGCTCAAGGAGTTC
CTGGGCGAGCAGCGGCGGCGCGGGCTGAGGCTGCCACCCGCCACAAGGTGCTGCTGCGC
TCCTACCCTGGCGGCCCCCTAGAGGCACGGACCACAGCCAGGCCTCGGGCTTCAACTGGGG
TTCCACCAATGCCACGGGACATTCCAGGGCCACGCTGAGCCAGGCGGGCCTGGGGCTT
CGGTTACCACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA
GACCCAGGGCCTGGACCTGATGCCACCCAGGCCAAAGCCAGAGTGGGAGACCCATTGG
TCAGGCTCAGCAGGGTGGGAACAGGCAGAGGGACAAGAGGGGAATGGAGAAGTGGAGAGG
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTGGGGGTGAGT
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC
CCAGGTGTCAGGGCAGTAGGCTGGGAGTCAGTGTGGCAAAGCGGGGGCAGGACACAGATA
CAGTGGCAGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGGCGGCAGAGGGAGAAG
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGCTGTCAGCATCCCTCAGAGGAGAAATGTG

62/113

FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCTCCTGTCCAGTGGATACAGC
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCTCCATGGCCTTTGGCCTTCT
TCCCATTCATATTTATTTATTTATTGACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT
ACTGCCCATGTTGTCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA
AGGAAATAAAATGGCAAGCAGCAAAAAA

SEQ ID NO: 43_AA542015_M SGK088_M

GCCACGGACATCTGGGGAGCGGGTGTGCTCACCTACATCATGCTTAGTGGGTACTCCCCA
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGGTCTGCTTTGATGCC
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGGTCTCTCA
GTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCACCCATGGCTGCAAGAT
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTCACCACCAACCGGCTCAAGGAA
TTCCTGGGCGAGCAGCGGCGACGTGCGGCTGAGGCTGCTACCCGTACAAGGTGCTGCTC
CGCTCCTACCCTGGCAGCCCCCTAGGTGGCACAGACCGCAGCCCGGCCACGGGCTTCAACT
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTACCCCGGCCATA
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAAGA
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT
TAGGCTGGAGTGGAATGCTATATCTCAGGGAGAAGCCAGAAGGGGACATGGCTGAAGAGG
AAGAAGGACCCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC
CAGGAGCCAGAGCAGAGACATAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAAG
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC
ACTGGCCAGGGATGTCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCCATTGTAT
TTATTTATTTATTGCCTTTTGTGGAGTTTCCTTTCTATCCAGTCCCTAGTGCCTATGTTG
TCCCGACCATCCCCCTTCAGTCACCCAGCTGTCTGTGCAGCTGTCTGTCTGTCTGTCTCA
AGGAAATAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAGC

SEQ ID NO: 44_R19772_H

ATGAAGGGCGGCGACAGGGCTTACACCCGAGGTCCCTCTTTGGGGTGGCTCTTTGCTAAG
TGCTGCTGTTGCTTCCCGTGTAGAGATGCATACTCTCATTCCTCAAGCGAGAATGGAGGC
AAGTCCGAGTCCGTAGCCAACCTGCAGGCCAGCCCTCCCTGAACCTTCATCCACAGTTCC
CCGGGTCCCAAGCGCTCCACCAACACTCTTAAGAAGTGGCTGACGAGTCTGTGCGTCGG
CTCAACAGCGGGAAGGCAGATGGAAACATCAAAAAGCAGAAGAAAGTTTCGCGATGGTCCG
AAGAGCTTTGACCTGGGATCTCCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCACACACACCC
CTCCCACCACCTATGAAGATTTTTTGACAACGACCCTACACAGGATGAAATGTCCTCCTCT
TTGCTAGCAGCCCGGCAGGCTTCCACTGAAGTACCTACTGCTGCAGACCTTGTCAATGCA
ATAGAAAAGTTGGTCAAAAACAAGCTGAGTCTAGAAGGAAGCTCATACCGGGGGAGCTTG
AAAGACCCTGCAGGCTGCCTGAATGAGGGGATGGCCCCACCCACACCTCCTAAAAATCCA
GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGAATGAGCTGGTA
CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA
ATAGAAGAAAAGGGTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTTTGGAAAT
ATTCATCAGATTTATGACTGGCATAAGGATTTTTTCTGCGGAACTGGAAAAGTGTATC
CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCCTAC
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGACTTCCTCATCAAG
CCCATTCAGAGAATAACAAAATACCAGTTGCTCCTCAAGGACTTCCTGAGATACAGTGAG
AAGGCTGGTTTGGAGTGTTGAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTC

FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG
CAGTCCCGGACCAAAGAGAGGGCGCGTGTTCCTCTTCGAGCAGATTGTTCATCTTCAGTGAA
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAAGGAGCATCAAGATGAAT
TACTTGGTCCTGGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACCTCATGAACAGA
GAGACTTCTGAGAGGGTTGTTCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTTGAATGCACTGCAATCGCCC
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT
CCCCAAGCCAGCCCCAGGCCCTACTCCTCTGTTCTGCGGGCTCAGAGAAGCCCCCAAAG
GGCTCCAGCTATAACCCACCTCTGCCTCCCCTGAAGATATCTACCTCCAATGGCAGTCCA
GGGTTTGAATACCACCAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCCTCGCCGTCAACCAGCAGAACATGTGT
CTGGTGTACCAGCCTGCCAGCGACCATTCCCCCGCCGCGAGGGCTGGGTCCCAGGCAGC
ATCCTGGCGCCCCCTACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG
TCATGTTTCATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGAGAAACACGGGTAAA
AATGAAGCCACAGGGCCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTTAAA
GAGACGAACAGTTCCGAGGAATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG
ATCTTAAATCCAAATTTTCATCCAAGAAGTGGCCCCAGAATTCCTTGTGCCCTTGGTGGAT
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAAG
CCCACCATCACTTGGAAGGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC
ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCTGAAGATCTGTAATCTGATG
CCCCAAGACAGTGGGATTTATACCTGCATAGCAACAAATGACCACGGGACCACATCAACG
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCCAGGAG
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAAACTGCACT
ATTTCTGGTTACACTGTGGAGTACAGAGAGGAAGGTTCTCAGATCTGGCAGCAGTCAGTG
GCTTCGACCTTGGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGGTGTCTTATCAG
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCCAGCGAGCCCTCGGAGTTT
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCATTTCTTGGAAGGAAAAT
TTTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCCGTTTCTCTATAGTAAAG
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTAAACAAAAAATG
AAGAAGAAAGAACAGGCTGCCCACGAGGCTGCCCTGCTTCAGCACCTACAGCACCCCCAG
TACATCACTCTCCATGACACCTATGAGTCCCCCACATCCTACATCCTGATCTTGGAAGT
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAAA
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACAAGTGCAGGGTT
GCACATTTGGACATAAAGCCTGAAAACCTGCTCATTGACCTACGGATTCCAGTGCCTCGA
GTGAAGCTCATTGACTTGGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTACCAC
CTGCTGGGGAACCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTCATGCTGAGTGGGGTCTCCCC
TTCTTGGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTAGCTTC
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTTCATCAATGTGATCTTA
CAGGAAGATTTTCGGAGGCGGCCACAGCAGCCACATGCTTGACGATCCATGGCTGCAG
CCCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCCTAGCATGCTTCATA
GAACGTCGCAAGCACCAGAATGATGTGCGGCCTATCCCCAATGTCAAGAGCTACATTGTC
AACCGGGTGAACCAAGGGACGTAG

SEQ ID NO: 45_5R72_8_2_H

CGCCGCTGTTTGTCTCGCGCGGCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA
AAGTTTCTCCCGGTGCAGAATTCGGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT
GTCGGAGACCCGCCAGTCCGCCGGCCCCGGCTTTGTTCTGTCGGAAGTGTAGTGGTGAGA

FIGURE 2KK

AAAACCTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC
TGGGCTGTACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAGTTC
GAAATTACAGTTTTTACCATCAACTACCTTATCCTTTTTTGGCCTGGTTTTCTTCCTCAAA
CAGTGGAAACATTTTTAAAGTTGCTTTTGTGTGCAGAGTTAAACAAATGGCTGATAGTGGC
TTAGATAAAAAATCCACAAAATGCCCGGACTGTTTCATCTGCTTCTCAGAAAGATGTACTT
TGTGTATGTTCCAGCAAAACAAGGGTTCCTCCAGTTTTTGGTGGTGGAAATGTCACAGACA
TCAAGCATTGGTAGTGCAGAATCTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA
GCATCTCAGCAACAATGGGGTCGGGGCACTTTACAGAAGGAAAAGTTCTTCACATAAGG
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTTGAAGAATATTGGGAAAAGGG
AGCTTTTGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTAAA
AAAGTGAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC
ATTCTGAAAAGTGTAACACATGAACACATCATACATCTGGAACAAGTATTTGAAACGCCA
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAACTCAAAGAAATTCTGGAT
AGGAAAGGGCATTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAATATAATG
GTTAAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG
ACTCCTATCTATATGGCCCCCTGAAGTTATCAGTGCCACGACTATAGCCAGCAGTGTGAC
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCTTTTGGCA
AGCTCAGAAGCGAAGCTTTTTGAGTTAATAAGAAAAGGAGAACTACATTTTGAAGATGCA
GTCTGGAATTCCATAAGTGACTGTGCTAAAAGTGTTTTGAAACAACTTATGAAAGTAGAT
CCTGCTCACAGAATCACAGCTAAGGAACCTAGATAAACCAGTGGTTAACAGGCAATAAA
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAAATAACCCA
GAAAGTGTTGAGGAAAACACAACAGAAAGAGAAGAATAAGCCGTCCACTGAAGAAAAGTTG
AAAAGTTACCAACCCTGGGGAAATGTCCCTGAGACCAATTACACTTCAGATGAAGAGGAG
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCTCTGCAACCAGTAAGGACAACCTTTGAT
ATGTGCAGTTCAAGTTTCACATCTAGCAAACCTCTTCCAGCTGAAATCAAGGGAGAAATG
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC
GCCCTGTCCAGAACCAAAAAGAACTCTAAGGTTCCCTCCAGTGTTGGACAGTACAAAAA
CAAAGCTGCTCTTGTTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG
CTGAGCTTGTAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTTGCACCAGCTTAAAT
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAAGGACAGCCACCAG
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTACTTCAAATTCT
TATGTTTAGGCACAGCTATTTATAGGGGAAAACAAGAGGCCAAATATAGTAATGGAGGTG
CCAAATAATTATGTGCACTTTGCCTAGAAAGACTTTGTTAGAAAATTACTAATAAACTTG
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTACATGTGTTCTGTGAGATTTTAGGTT
GCTATAGATTGTTTAAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAACTG
CTTGCCATTAACTTGCTGCTAAATTCCCAATGTATTGATTAAATCAATAAAAAACAGATG
TTACTC

SEQ ID NO: 46_SGK309_H

GGGTCCGCAGCCCGCCCTCACAGGCCCTCCTCACTCCCCTAGGTAGATGGCCCCCTCAGG
GCAGGCCCCGGCGGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCGCCCTT
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCCTGCCGGCCAACTAC
GTGGTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGGCTTTGGTGAGATC
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCCAAG
CAGCCCAAGCAGGTCCCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTTCGGGC
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGGAAGGAC

65/113

FIGURE 2LL

CATGTGTGCAGGTTTCATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG
AGCACCACATTTGCGGCTGGGCAAGCAGATCTTGAGTCCATCGAGGCCATCCACTCTGTG
GGCTTCCTGCACCGTGACATCAAGCCTTCAAACCTTTGCCATGGGCAGGCTGCCCTCCACC
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG
GATGTGCGGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTCGCTATGCCTCAGTC
AATGCCCAACAAGAACCGGGAGATGGGCGGCCACGACGACCTGTGGTCCCTCTTCTACATG
CTGGTGGAGTTTGCAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA
GGGATGATCAAGGAGAAGTATGAGCACC GGATGCTGCTGAAGCACATGCCGTCAGAGTTC
CACCTCTTCCTGGACCACATTTGCCAGCCTCGACTACTTCACCAAGCCCGACTACCAGTTG
ATCATGTCAGTGTTTGAAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT
GACTGGGAGAAGGCAGGCACCGATGCCCTCCTGTCCACGAGCACCTCTACCCCGCCCCCA
GCAGAACACCCGGCAGACCGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCTGG
GGACCTGCTCCGGGAGAACACCCGCGGATGTGCTACAGGGAGAGCACCTGAGTGACCAGGA
GAATGCACCCCCAATTCTGCCCGGGAGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT
TGTCCCCCACCCCGGGGGTCTTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA
CAAACCTCCGGATCAACATCGGCAAAGTAACTGCCGCCAGGGCGAAGGGCGTGGGTGGCCT
TTTCTCTCACCCCGATTCCCAGCCTTGTGCCCTTGCCCTGTTCTCCTAAGCACCTGT
CCCCCGCCAATCTCCTGCTTGCCCGGCCCTCTGTTTCCGGTCCCCTCCCCGGCACTAGCC
TCGCTGTGTCTTCCATCATCATCCTCTGTCTCCTTCACACTGAGGAGACCATCCGCC

SEQ ID NO: 47_AA234451_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAACAGCAGC
AGCAGCCGCGCGCCGCGCCGCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCGCCGAGTCGGCGGTGGGGGATGGGCAGGCA
GTGGCGGTCCCGCTGCCGAGGGTTAACCCCGCCGGTCCCGGTCTTGAGCTGGACCAGA
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCAGGTTAAATGGAAACCACCCTTGG
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA
GAGCAGCTGGATATCCTGAGTGTGGAATCCTAGTGAAAGAAAGATGGAAAGTGTGAGA
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGACATGCTCACCAGGGAA
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT
GCTGTTTTGAAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTTATTGGCTGTGGGAGG
AATGATCGATTCAACTATGTGGTCATGCAGTTGCAGGGTCGGAATCTGGCAGATCTTCGC
CGTAGCCAGTCCCGAGGCACATTCACCATTAGTACCACTCTCCGGCTGGGTAGACAGATT
TTGGAGTCTATTGAAAGCATTCATTCTGTGGGATCTTGNCATCGAGACATCAAACCGTCG
AACTTCGCTATGGGTCGCTTTCCTAGTACATGTAGGAAATGTTACATGCTTGATTTTGGC
TTGGCTCGACAATTTACCAATTCTGTGGTGACGTCAGACCACCTCGAGCTGTGGCAGGT
TTTCGAGGGACAGTTCGTTATGCATCAATCAACGCACATCGGAACAGGGAAATGGGAAGA
CATGATGACCTTTGGTCCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCCC
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAGGAGAGATATGACCACAGG
CTCATGTTGAAACATCTCCCTCCAGAATTCAGCATCTTTCTAGACCATATCTCTTCTTTG
GATTATTTTACAAAACCAGACTACCAGCTTCTTACATCCGTGTTTGACAATAGCATCAAG
ACTTTTGGAGTAATTGAGAGTGACCCTTTTGAAGTGGGAGAAGACTGGAAATGATGGCTCC
CTAACAACCACCACTACTTCTACCACCCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAAATACAGATGAG
GTATTTCCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA
GATAAATTGCCTGGATCTCTGGGACACCCCGTCCCCAGGAGAAGGATGTTTGGGAAGAG
ATGGATGCCAACAACAAACAAGATAAAGCTTGGAAATTTGTAAGGCTGCTACTGAAGAGGAG
AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTTGGGTACCAATTCTG

FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCACTGGTGCGAAAGTTACGTTCC
ATTCACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG
TTCCTTGAGACCTGGTATAAAATAGTGTATTTTTCTTTTTTAAAGCTTCTAAGGTACCATT
ATTATTGTTGTCATTGTTGTTATTATTATTGTATATTTCTGTTACATAAAGTCTTTCAA
TAAGAAATCCTTGCATTTTTTGTAACACTGAGTCTATTTCAGCTCCAATTTTCATCCATGTT
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCCTAACACTAGGTACAAGTTAAATGAACAT
TTTTACAGTAACCTTTGTTTAGAAAGTAATCTCTTCCACACAACAGTGTAGTGCTGGAGAG
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT
AATTCATACACAAGGGACGGTGAGTTCAATTCACCTTAGTGAAGACCCTCTAGGAGTAAG
ATACTGTGGGAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG
TGCATGGTTTTGAGGCACATTATCCCTACAACAAATTTTGATAACAGAAGAC

SEQ ID NO: 48_AA435956_H

ACTTTTACTATATTCTTTGAGATGACTGTTTTTGATTTAGAGGCGAAATCAGCACGTGGT
GGCTCAAATCTCCTTATGGATAGTGTTCCTTCCAGCTTTTCATGTTTCAACTTTTG
CGGGGCTGGCGTACATCCACCACCAACACGTTCTTCACAGGGACCTGAAACCTCAGAAC
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCGGGCCAAG
TCCATTCCCAGCCAGACATACTCTTCAGAAGTCGTGACCCTCTGGTACCGGCCCCCTGAT
GCTTTGCTGGGAGCCACTGAATATTCCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCTGGGGTTTCCAACATCCTTGAACAG
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC
AAGCTACCTAACTACAATCCAGAATGGTTCCCACTGCCTACGCCTCGAAGCCTTCATGTT
GTCTGGAACAGGCTGGGCAGGGTTCCTGAAGCTGAAGACCTGGCCTCCCAGATGCTAAAA
GGCTTTCCCAGAGACCGCGTCTCCGCCCAGGAAGCACTTGTTTCATGATTATTTTCAGCGCC
CTGCCATCTCAGCTGTACCAGCTTCCTGATGAGGAGTCTTTGTTTACAGTTTCAGGAGTG
AGGCTAAAGCCAGAAATGTGTGACCTTTTGGCCTCCTACCAGAAAGGTCACCACCCAGCC
CAGTTTAGCAAATGCTGGTGAAAAGAAAGGGCGAGATCACCAAGGTTCTTCCAGGGCTGT
ATTTCTGCAGTTTCGGTTTTTCATTGCTTCAGCTTACTAAGAAGCTTCAAATCTAACTCC
ATACTGAACAAGGGGCTTTATGTCCTCACCTATGACCTGGAATAGTTTAAATATGGTGT
CAAGGCAATAGTACATAATAGTGGAAGAAAATTCAGTGGAAGGTTATTGCTATTGTCATT
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAACTAAGTCTAAGAAG

SEQ ID NO: 49_AA626859_H

AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA
TTTCTGTATATACATAACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAAC
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA
TGCTTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGA
TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCT
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA
TGGCATCAGTATACCTGAGCCAGAAGACATGGAACTCTTGAGGAAAAGTTCTCAGATGT
TCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAA
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAACAAGTCTCCAGTTAAA
ATTTGATCACCTTCCAAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT
GTACACATTTTGTACAAGTGAGATAGGAATTCTCAGTGTTTCAAATGCAAATGAGCCATA

67/113

FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCCCTTTCCCCA
TGCTTTTACAT

SEQ ID NO: 50_AA061797_M

GAAAATAGCCCTGCGGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT
CATCGAGGTGTTTCAAGAGAAAGAGAAAGATGCATCTAGTTTTTGAGTACTGTGATCACAC
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAGTGT
GCTATGGCAAACCTTCAAGCCCTTAACCTTCTGTCAAGCACAATTGTATTTCATCGGGA
TGTAACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG
ATTTGCACGAATTCTAATTCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA
CCGAGCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGC
CGTCGGCTGTGTTTTTGAGAGCTCCTGACGGGTACGCCACTCTGGCCGGGAAAATCCGA
CGTGGACCAGCTTTACCTGATCATCAGGACGTTGGGGAAGCTGATTCGAAGACACCAGTC
TATCTTTAGGAGTAACAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA
GACTCTTGAAGAAAAATTCTCAAATGTTTCAAGCTGTGGCTTTAAGTTTCATGAAGGGATG
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCAGCTGCTGGACAGTGCCTACTT
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAAAGCCGAAG
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCTGGAAGCCACATCTCCCCACACCTGA
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTTCGATCATCTTCAAACATTTAGGGGACTCA
TCCTTCCCAGCACATCCTTTTAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA
TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC
CTGTGCTTTTTCCACGCCAGCTCCATCTCCTAAAACATTCTCTTTAAATGTTGCAGTATC
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTCACCAGAGCCGGGCTTCCTCAGGCAA
TCGGTACTGTGCATCTGTGGACTTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT
CTCACTTCAGCCGACCAGTGGTGTCTGAAGCAGACCCAGATCTGCTGGCTGCTGTTTGT
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT
TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA
CGAACTAGAGAAAAATTCCAAACGTGACCAGTTAGTGGACAGACTACAAGGAATCGACCAC
CATACCACAGTAACGCCCCCTGGATCCCTGGCTGCCCCACCCACTCTAAGGCTATCCTGGTT
CACCATGGTTTCTCTTTCTTTTCTTCTTTTCTTTTAAATCTATTTGTACATATGAGAAAGAGG
AGAGGGGCGAGAGAAACCTCGTGTGTGAAATCAAAGACAAGCAGGAGGCCAGCCTAAG
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCCAAAGTCCCT
GCTGCTGATTGTATAAACTATGAATAAGTTCTACATATGTAGGACATATTGTTGTCATTG
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTTCTAAATATTCTCCACACTGGTG
AGTATCTTGGCATTTCATTTCTGACCTCATCACAGATGAACACATCAAAGGATGAGTATG
TATCACTTTGCATCTTAGAATTCTACCTGTTTTAGCTGCGTTAAACCTTGTGAAAGGGCG
GGGCCATAACTGAACCTGTGGAGTTCTTGCCTGTGTGCAGGAAACCTCTGGTTTTGTCT
CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAATTCAAAGTCACT
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG
TCCGTGTTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC
ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAACCTAATAGGAGTCGTTGAAGGTAG
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTAGTTTAGAAT
GCATTAATGTATGTAGAAGCTGGGCTATTTTCAGATTATTTGAAATTGTAGCTATTGTTAA
TTAGCACTTAATAACTAAGTAGCATTATGGTAGTCTAAACTATTAGAGTTTACTACAAAG
AGGTTTTGATTGAATTATATAAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA
GAAAGCTATATAAAGATTAAACATTTTTGTGGCTGTATATTTGTGTATATACCTTGGTTG
TTCTTTAAATTATTTTAATAAAAGCCAGAAACATT

68/118

FIGURE 200

SEQ ID NO: 51_AA397553_H

ATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGA
TTGCGAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTG
GATATCGAAGCACAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGAC
CCCCGAAGCAGCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATAT
CAGCTCTGATTCCGACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGG
GAGAACGACGACGACGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGC
ACAGGCGTTCCCGGACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAGCCAAGA
AGTCTCCAGCAAGTCGGATCGATGAAGGACCGGATATCGGGAAAGTTCAAAGCGTT
CGAATGAGGAGACTGATGACTATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAG
GAATCCAGGTCATCCAAGCTCCACAAGGAGAAGACCAGGAAAGAACGGGAGCTGA
AGTCTGGGCACAAAGACCGGAGTAAAAGTCATCGAAAAAGGGAAACACCCAAAAG
TTACAAAACAGTGGACAGCCCCAAAACGGGAGATCCAGGAGCCCCACAGGAAGT
GGTCTGACAGCTCCAAACAAGATGATAGCCCCCTCGGGAGCTTCTTATGGCCAA
GATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGACTCCTACA
AGAAAAGTCTTGGAAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG
GAGCCTTCGGCCTACCAGTCCAGCACCCGGTCACCGAGCCCCCTACAGTAGGCGA
CAGAGATCTGTCTAGTCCCTATAGCAGGAGACGGTCGTCCAGCTACGAAAGAAG
TGGCTCTTACAGCGGGCGATCGCCCAGTCCCTATGGTTCGAAGGCGGTCCAGCA
GCCCTTTCTCTGAGCAAGCGGTCTCTGAGTTCGGAGTCCACTCCCCAGTAGGAA
ATCCATGAAGTCCAGAAGTAGAAGTCTGCATATTCAAGACATTATCTTCTCATAG
TAAAAAGAAGAGATCCAGTTCACGCAGTCGTATTCCAGTATCTCACCTGTCAAG
GCTTCCACTTAATTCAGTCTGGGAGCTGAACTCAGTAGGAAAAGAAGGAAAGAG
CAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCCAAAGGGTTCACCT
GTATTTTTGCCTAGAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTCAAGTTT
GGAGTCTAAAAAGTTACCCAGAAGTGTAATAATTGGAAAAATCTGCCCCAGATA
CTGAACTGGTGAATGTAAACACATCTAAACACAGAGGTAAAAAATCTTTCAGAT
ACAGGGAAAGTAAAGTTGGATGAGAACTCCGAGAAGCATCTTGTTAAAGATTTG
AAAGCACAGGGAAACAAGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGT
TACTCCAAAGGAGACAGAAACAATCAGAAAAGGAGACCCCTCCACCTCTTCCC
ACAATTGCTTCTCCCCACCCCTCTACCACTACTACCCCTCCACCTCAGACAC
CCCCCTTTGCCACCTTTGCCTCCAATACCAGCTCTTCCACAGCAACCACCTCT
GCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCCCTGCTTCCAGTACTTCAACT
TTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGTCTCTCAGGCAAAT
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAAACAGCT
GCTATTCCACACCTGAAAACCTTCAACGTTGCCTCCTTTGCCCTCCCACCTT
ATTACCTGGAGGTGATGACATGGATAGTCCAAAAGAACTCTTCCTTCAAACCT
GTGAAGAAAGAGAAGGAACAGAGGACACGTCACCTTACTCACAGACCTTCCT
CTCCCTCCAGAGCTCCCTGGTGGAGATCTGTCTCCCCCAGACTCTCCAGAACC
AAAGGCAATCACACCACCTCAGCAACCATATAAAAAGAGACCAAAAATTTGTT
GTCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGGAAACGCTGT
GTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGT
GAGACTAGACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTCTGTGAAATCA
AAATCCTTCGTCTAGTTAATCCACCGAAGTGTTGTTAACATGAAGGAAATTGT
CACAGATAAACAAGATGCACTGGATTTCAAGAAGGACAAAGGTGCCTTTTACCT
TGATTTTGAGTATATGGACCATGACTTATGGGACTGCTAGAATCTGGTTTGGT
GCACTTTTCTGAGGACCATATCAAGTCGTTTCATGAAACAGCTAATGGAAGGAT
TGAATACTGTCAAAAAAGAATTTCTGCATCGGGATATTAAAGTGTCTAACAT
TTTTGCTGAATAACAGTGGGCAAATCAAACCTAGCAGATTTTGGACTTGCTCG
GCTCTATAACTCTGAAGAGAGTCGCCCTTACACAAACAAAGTCATTACTTTGT
GGTACCGACCTCCAGAATACTGCTAGGAGAGGAACGTTACACACCAGCCATAG
ATGTTGGAGCTGTGATTTCTTGGGGAATAATTACAAAGAAGCCTATTTTTCA
AGCCAATCTGGAACCTGAGCTAGAACTGATCAGCCGACTTTGTGGTAGCCCT
TGTCCAGCTGTGTGGCCTGATGTTATCAAACCTGCCCTACTTCAACACCATG
AAACCGAAGAAGCAATATCGAAGG

FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTTCATTCCTTCTGCAGCACTTGATTTATTGGACCACATG
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT
AAAGATGTCGAACTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCAT
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTGTAGTCGAAGAGCCA
CCTCCATCCAAAACCTTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG
AACAGCAGCCCAGCACCCACCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG
ACGGAAGCTACTTCCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG
GAAGCACCCCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCCTGAAGCTTCA
AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG
CCCCGAAGAACTCCCACAATGCCACAGGAGGAGGCAGCAGCATGTCCTCCTCACATTCTT
CCACCAGAGAAGAGGGCCCCCTGAGCCCCCGGACCTCCACCGCCGCCACCTCCACCCCT
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC
TTGCTGCAACTTTTATCCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC
ACTGATGGGCCTGAAACAGGGTTTCAGTGCCATTGACACTGATGAACGAAACTCTGGTCCA
GCCTTGACAGAATCCTTGCTCCAGACCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAAGTTTCCAGGGGAC
CAGGACCTCCGTTTTTGCCAGGGTCCCCTTAGCGTTACACCCGGTGGTTCGGGCAACCATT
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAAATTGCAAAACTAT
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG
GGCCCAACTCAGTCTTCTGCTTATGGAAAACCTCTATCGGGGGCCTACAAGAGTCCCACCA
AGAGGGGGAAGAGGGAGAGGAGTTCCTTACTAA

SEQ ID NO: 52_AA789239_H

TGAAATGGAGATGTATGAAACCCTTGAAAAGTGGGAGAGGGAAGTTACGGAACAGTCA
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAAGATATTTTATGAGAGAC
CAGAACAATCTGTCAACAAAATTGCGATGAGAGAAATAAAGTTTCTAAAGCAATTTTCATC
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCATTTGGTAT
TTGAATTTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTTCATGGACTAGAGA
GTAAGCGACTTAGAAAATACCTCTTCAGATCCTTCGAGCAATTGACTATCTTCACAGTA
ATAATGTAATCATTTCATCGAGATATAAAACCTGAGAATATTTTAGTATCCCAGTCAGGAA
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAAAGATACTTCTT
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA
CTGGAAATCCCTATCTTCCTAGTAGTTCTGATTTGGATTTACTCCATAAAATTTGTTTTGA
AAGTGNGATTTCATGCCAGAACTGAAAGCTAAATTACTGCAGGAAGCAAAAGTCAATTCAT
TAATAAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAAACAG
TTTATACCAATACACTGCTAAGTAGTTTCAGTTTTGGGAAAGGAAATAGAAAAAGAGAAAA
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAAGTCAAAGGAGGAAGAGGAGATATCTCAG
AACCAAAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTC
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATTGAACCACCAAACCCTATCAATCCCA
GCACTAACTGTAATGGCTTGAAAGAAAATCCACATTGCGGAGGTTCTGTGACAATGCCAC
CCATCAATCTAACTAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTACC
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAAGAGACGCACCTTCTTCACAATCTATTGGAC
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCCTATTCAAAGCCAAATGGAGAAGG
GTATATTTAATGAGCGAACAGGTACAGTGACCAAATGGCAAATGAGAACAAAAGGAAGC

7-2/113

FIGURE 2QQ

TGAATTTTCCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC
AAGAGTTTATTCCTTATCTCTGCTGTCTGCCTGCTGTCTTATTTTACAAATATTTGCT
CTCAGCTAACTATCAGGCTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG
GTTTTTTTTCTGGTAGTGTCTTTTCTTTTACATAGTCCAAAAAATAACAAGATGACAACTC
TTCCCGTTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC
ATGTGCATGAGCATCATCCAGCTTTTTTTGTTAGCAAAACATTTACTGTTTTCTTTTCCC
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC
CTTGAA

SEQ ID NO: 53_AA124976_M

CTGGCAGATATAGTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT
GATCTTTTGCCTCACGATTACTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCCAGACCAGAAGAAGCCA
GAGTATGAAGGCGACACCAGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCCAGTGAGAATTCTGAC
GGTGTCAAAGAAGACCCACACGCTGGGGGTGTATGATAATGCCACCTATCAACCTGACA
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCCACCCCAATTCACGGTTA
ACTGAAAGAACAAAAAGAGACGCACCTTCTTACAAACTATTGGACAGACTTTGTCTAAT
AGCAGACAAGAGGACACAGGTCCCACACAAGTCCAAACAGAGAAAGGTGCATTTAATGAG
CGAACAGGTGAGAATGACCAAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA
TGCGACAGGAAAGAATTCCATTTCCCTGAACTGCCATTTCACAGTGCAGGCGAAGGAGATG
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTCCCGATAGTGCTTT
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTTATTTTATATAC
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT
CTATTTTTTTGGTTTTGCTAGCAAAATTTTACAATTTTTCTCTATCTTCCAAAACTGT
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG
AGACTCAAACCTCATAAGCCAGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA
CATTCTATTGTCCCCAGTGAAGCATTTATAGTACTTACATAACATGTTACAGTGATATGA
TGTTCCTAGGTAAACTCCTTGAGATGAAACTATTTCCCTGCATTCTCTGACTCCCCTAGT
CTAATAGTTTCTTCCATTTAGCCAGAAGAATTTCCCTGAAGAAGCGATGCACAACCTGGGA
AAGGTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA
GTTAACAT

SEQ ID NO: 54_AA575635_M CCRK_M

AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCGGGTCTTCTCTCCGGAT
GGTGGTCGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACCTGTGCTGT
GTGCTTCGCATCCTGGGTACCCCGAGTCCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAAGTGCCCTGGAGGAGGTGCTGCCT
GATGCCTCTCCCCAGGCCTTGACCTGCTGGGCCAGTTCCCTCCTCTACCCTCCACGACAG

7/11/03

FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC
CATCCATCCGAGCTGCCAATTCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC
CCAGAACTGATTTCGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCCTTCTGCT
CGCCCTAGGAGCACCTCTTTCTGATTTGCCTCCATGGCCTCCCCACGGCTATATATACCA
CACCTGGTCTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCCTGAGA
TGTTTCATCCCAGCAGAGAAAGAGACTCACGTCTTACAGACAAAGCCTCCAGAACTGCTA
GCTGTGTCTCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC
AGGCTCTGTCCCCTCTTCAAGGACATTGGTACTACAGCACCACTGGTGGAAGCACAGAG
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT
CCACTGGGTCAGGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTCTGTCTAATTGCACC
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTACAGGGGTCAGGTACT
CAGAAGGGGCTCCTGTGAAGGCCATTTGGGTCTCAGGCTTCCCATGCTATTACGGGA
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCAGGGATGGACAGTCCAG
TTCCCGAAGCCCACTTCCCACATGTGCGGTGGGTGAGTCAGTGAGCCTGAGGCTGCCTTG
CAGATGCGGAAGCAGGCATTCTTGAATCCACTCAGTAAATAAATTCCAGTGTGACTCAG

SEQ ID NO: 55_AA631990_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA
TCTGGTCACACTCACTATCCATTTCATGATTACAACCTCTTCAATACTATCGCGGCCGAGGA
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTTCGGGAGATG
CGGCATTCCAAAAGAACTCACTGTCTTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTCATTATTTAGAAGCAAGGTCC
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT
GAAGGATATGTTCTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGC
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGT
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGC
AAAGTTGTAGAGTGCAATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAAATCGTA
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTGAGAAATCCAAGTATTAGAGCACTTA
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT
CATGGTCATGTTTGTATTGTGTTTGAACACTACTGGGACTTAGTACTTACGATTTTCATTAAA
GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAATGAAACGTGATGAA
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
CTTGGTTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
ATATTAGGACCCATACCACAACACATGATTTCAGAAAACAAGAAAACGCAAGTATTTTTCAC
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC
AAACCGTTGAAGGAATTTATGCTTTGTGTCATGATGAAGAACATGAGAACTGTTTGACCTG
GTTTCGAAGAATGTTAGAATATGATCCAACCTCAAAGAATTACCTTGGATGAAGCATTGCAG
CATCCTTTCTTTGACTTATTAATAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA
CTTCTCTAGAAGAGATTACTTAAGACTGTGTGTCAGTCAACTAAACATTCTAATATTTTGT
AAACATTAATTTATTTTGTACAGTTAAGTGTAATATTGTATGTTTTGTATCAATAGCAT
AATTAACCTTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAATAATTTT
TCTTTTGAATTAACATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT
GTGATTGATCTTGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTTGTAGTAAA
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

72/113

FIGURE 2SS

ACTTAACTTTAAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAG
ATAAGCAGGTACTAGAAACCAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT
TTAAGTGTGTATTCTTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACACATACACACTTTATTT
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAATAATGGACATTTCCAAGTATGTTTGGT
GAGTCACAGATATAAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTAT
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA
TTGGTTACATAAACTTTTTGACTTCAAT

SEQ ID NO: 56_AA557536_H

AGTAAGGCCCCGCGGCGTCCTGGCCGCCATGTGCACCGTAGTGGACCCTCGCATTGTCC
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCCTCCTGGCCTTCCAGCC
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTTTGAGTTTATGGACACTGACC
TGAACGCAGTCATCCGGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT
ACCAGCTCCTGCGGGCCACCCGTTTCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCTGAGGACCAGGCCGTGACAGAGTACGTGG
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTTTCGCACCGCTACACCGCTTCCT
GCCCCAGATACACCCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC
TGCGGGGGAGACCCCTGTTCCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG
AGACCATCCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC
CGCCAGACACCTCCCCAGAGGCCTTGACCTCCTTAGGCGACTCCTGGTGTTTCGCCCCGG
ACAAGCGGTTAAGCGCGACCCAGGCACTGCAGCACCCCTACGTGCAGAGGTTCCACTGCC
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCCGGGCACACGAAGGGGTCCAGC
TCTCTGTGCCTGAGTACCGCAGCCGCTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA
GCGGCACCTCGAGAGAGAAGGGCCCCGGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA
AACCCAGAGCCGACCCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC
CCCAGAGCAGCCAGGCCATGACCCTGCCGAGCACGAGTCCCCCGGTGCAGCCAAGAACG
TTCCAGGCAGAACTCCGCTCCCCTGCTCCAAACTGCTCTCCTAGGGAATGGGGAAAGGC
CCCCTGGGGCGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG
GAGCTGCGCCCTCCCTGACCTCCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC
GGGGTGACTGGAACCGGGCGGTGGGGTGAGGGTGGCCAGCGTACAACAGGTCCCTCCCC
GGCTTCCTCCGGAGGCCCGGCCCGGAGGATGTTTCAGCACCTCTGCCTTGCCAGGGTG
CCCAGGGGGGTGCCAGGGCTTTGCTTGAGGGCTACTCCCAAGCCTACGGGACTGTCTGCC
ACTCGGCACTGGGCCACCTGCCCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC
CTTACCTGGCCCTCTGTTCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCGTTGAAGTTCCAGGGAGCTTGCCCGGGT
CTCCTCGGGGGAGCAGATGAGGGCCCTGCCC

SEQ ID NO: 57_N28606_H, MOK_H

ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAAACGTTTTCTGAAGTTATGAAG
ATGCAAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAA
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGCACTA
ATATGTGAACCTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

73/113

FIGURE 2TT

TCAGAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTTCAC
AGAAATGGAATATTTTACAGAGATGTAAAACCAGAAAATATACTAATAAAGCAGGATGTC
CTGAAATTAGGGGACTTTGGCTCCTGCCGAGTGTCTATTCCAAGCAGCCGTACACGGAA
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCC
CTCTTTCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTCATCGGCACA
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCTT
TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCACCAGGCCCTG
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA
AAAGCTGGCTTTCCGGAGCACCCCTGTGGCACCGGAACCACTCAGTAACAGCTGCCAGATT
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA
CGAGGACCGGCCTATGTCATGGAACCTGCCAAACTAAAGCTTTCCGGAGTGGTCAGACTG
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG
CCGGTGTCTGAGACCCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC
CTTAAGCCTGCCCCGCAGCAGTGTGCGCTGCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58_AB023153_H, ICK_H

ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCTGCTG
GGAAGAAGCATTGAGTCTGGGGAGCTGATCGCTATTAAAAAAATGAAAAGAAAATTTTAT
TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC
AATGTAGTCAAATTAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG
TACATGAAGGAAAATCTTTACCAGCTCATTAAAGAGAGAAAATAAGTTGTTTCTGAGTCT
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTACAAACTCGGC
TTCTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA
ATTGCAGACTTTGGTTTGGCCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCCC
ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAAA
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACTTCCGTTGGCCACAG
TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACTTCGA
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCAACAAAACCTTCAGGATTCA
GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAGCCAGTC
CCACCTGCCCAGCCACCAGCCAAGCCACACACGAATTTCTTCACGACAGCATCAAGCC
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCGTTGCTTTTCCCATCCCTCCACAACAAG
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAATGGTGAGATAAAGCCAAAG
AGTAGGAGAAGGTGGGGTCTTATTTCCAGGTCAACAAAGGATTTCAGATGATTGGGCTGAC
TTGGATGACTTGGATTTCAGTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA
CAGAGTGATGACACTCTCTGCAGGTTTGGAGTGTTTTGGACCTGAAGCCCTCTGAGCCT
GTGGGCACAGGAAACAGTGCCCCCACCAGACGTCATATCAGCGGCGAGACACGCCCACC
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCCTGGGATCAGT
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCCACCTAATCCATGGTCT
AGTTCTGGCTTGTCTGGAATACTTTCAGGGACAATGTGAGTAATCAGCAAAGTAAATTCA
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAACTATGTCCCTTCTTTCTG
AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCAGACCCTTCC
CCTGGTTATTCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATTCTTGGACACC
CAGCCTAGAAGCACTCCTGGGTTGATACCAGGCCCTCCAGCCGCCAGCCAGTGCATGGC
CGGACAGACTGGGCTTCCAAGTACCCATCCCGGCGGTGA

FIGURE 2UU

SEQ ID NO: 59_AA839940_M

AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG
CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCCAG
GGCCCAGGAAGAAGCTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTTGAACACCGGGTAGTGAGCATCAAAGAT
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTCGGTTT
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG
CTCAGCCACGTAAACTTGATCCAACCTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTTGACCGGATCACGGATGAGAAGTAC
CACCTCACTGAGTTGGATGTGGTCTTGTTCACGAGGCAGATCTGTGAGGGTGTGCATTAC
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTCAGC
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATAACAAGCCTCGG
GAGAAGCTAAAGGTGAACCTTTGGTACTCCGGAGTTCTGCCCCAGAAGTTGTTAACTAT
GAGTTTGTGTCACTTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC
TGCAGCTGGGATTTTCGATGCTGATACCTTCAAAGGGCTGTGCGAGGAAGCCAAGGACTTT
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTTCGCTCAGATCC
CAACAACCTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC
CACTGGGCCTGGGAATTTCTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAATGATGGA
AGGAAGCAAGAAAGAAAGAAAGAAAGGGGGAAGAAAGGAAAGGCAGAAAGCAA
GGAAACAGGCTACGTTGTTGCTCTTCTGTAGGTGAAAGTGTTTTTATTAAGCCCTAG
GAATGTTTTTCTGCCTCGTAAGGTGAGCAGGTCTCATATGCTGCTTGCTACCCCGCACCC
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCCTACTTGGCTTT
TGGTCAAATTTGAATTCTAACTTGTATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA
TTCTTAAAGAATTAATAAAATATATTTTTTAAAGGAG

SEQ ID NO: 60_AA460132_H

GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAG
TGTCCGGGGTGGACGCATTTCGGGTAGCCGAAGAAGTCCAGGATTGCCGAAGAAGTCCCA
GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAGACAGCTGATCGGTTGGAG
CTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACGCGGCCGATGGCGAGGAG
CCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCGGGAGCGGAGCAGCCGCTTCTTGAGC
GGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGTTCGCTGGCCGCTTCCAGGGC
CGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGCTCCTCCGCTGTGCGCGCGCT
GGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCCAACCTGCTTATATATGGAA
GAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGTCCACTATGGAGACTGAAAAA
ACTCCCCAGGGTCTCTCCAACCTTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC
GATGAAGACCTCATTTCATGGTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCATTTTCAGCACTTCCAGAG
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCTCAGTACCCATCCCAACACT
GAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAAGGCCAGGCCA
GTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG
AAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAAA

FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTTAAGTGGTATGTG
ATCGTGTCAATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCCAGATTGTGACATGTA
TATCTCAGATAACATGGGTGTGGCATTGAACCACATAATGAGAAATATTCTCTTTTTAG
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT
AACCCAGTGTTTTTTTTTTGTTGTTGTTGTTGTTGTTATATTTATTTTGAAACCAGTTT
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61_SGK034_H

CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG
GACACGGAGGAGGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC
TTCGCGGCGCACGAGGAGAAGATCCAGACCGTGTTTCGAGCAGCTGGTGTCTGGTGGACCAC
CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGGTC
ATCTTCATCACAGAGTACGTGTATCAGGCAGCCTCAAGCAATTCTTCAAAAAGACCAAG
AAGAACCACAAGGCCATGAACGCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC
ACCATCTTCATTTCAGCACACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC
TCCAATGCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGG
AACCTGCACCTTCTTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC
ACCCGGGTCAAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG
CGGGAGTTCATCCTTTGCTGCCTGGCCCCGGGACCCCTGCCCGCCGGCCCTCTGCCACAGC
CTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC
TTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGAGGCCCCCGCTGCAGTGGCGG
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTCAGGAATGGAATC
TACCCACTGATGAACCTTTGCAGCCACTCGACCCCTGGGGCTGCCCGTGCTGTGGCCCCA
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC
AGAAAGGTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT
CTCACTCTGCTTCTGGTGTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC
CCAACGGACAGCGCCAGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCTTCCACGAG
GACGACCGGATGAAGCTGGCCGCTTCCCTGGAGAGCACCTTCCCTCAAGTACCGTGGGACC
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGCTGCCCGGGCAGGCC
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAAG
GCCCCGGTAGTGAAGGAACCCCCGCTCTCCTGAGAGTGGGGCTGACCTGCCTTGGGCGC
CGAGGGGTGGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCAGGTCTTACGATCAGG
GTTGCCCCCAGAACCCTTCCCATATCCTCCATTCTCCGCCCTGAGTTCTTACCCAGGCT
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCAGC
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCAGGGAAGTCTCCAT
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC
AGCAAGCCAGCGGTGACACACCTGCAGGTGTCAGGCATGGCACTGGGCACAACAGGGACC
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTGACGAAAGCCCCCT
GGTCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCCTGAGACCAG
AACTTGCAGCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCTCCAATGGGCTTTTTT
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC
TCACAGCCCTCCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCCTGGGCCT
CTGAGGATGTCAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCCCTGGCCTCTTGATTCTTGGCTT
GCCTCTCCTCCAATTCCAACTTAGTGAAATGGCCTTAAGCATTTTAAACTGTATGTATA
CATAGCGCATTCATGCCTTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC

76/119

FIGURE 2WW

TGTATTAGTTTTATACTGCCGCTGTAAAATTTACCACAAACTTAGTGACTTAACACAAAT
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG
CTGCTGGCAGAATCCACATCCTTTTCGGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC
TGTAACCTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCTTGCTCCTTGCCCC
CTCCTCCATCTTCAGAGCTAGCAGGTTCACTGTGTGTACGAACCATTTCTCTGGTTCCC
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT
GCCATGTAACTAACATTCCTGGTTCCAGGGATTAAGGAATGAACCTCTTTTGTGGGG
AAGGGTGGCATTCTGCTGACCACAGCACTCCAACCAAAGCCAAAACCAAAGCAAGACT
TACTAACGCATATCAAATAAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA
TTCCAATACTATTTACAAAATTATTCAAATCTCACGCCTTCCAACCTAAAATTAGCAAT
CTAAAGTAATTTCCATATCCTAGATGGAAACCTCATGCTAACTGTCTGATTATGCATG
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAACTGAACTTAA
AAGC

SEQ ID NO: 62_AA103218_M SGK034_M

CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG
GGAATTCATCCTCTCCTGCCTGGCCCCGGGACCCTGCCCGCCGACCCTCAGCCACAACT
CCTCTTCCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA
CCTCCATGCAGTTTTGGCTGAGATGCCGCAGCCCCATGGACCCCAATGCAGTGGCGGTA
CTCAGAGGTCTCCTTCTTGAGCTGGACAAATTCCTAGAGGATGTCAGGAACGGGATCTA
TCCACTGATGAACTTTGCGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC
CCCAGAGGAAGCCCAAAAGGCCAAAACCTCCAACGCCAGAACCTTTGACTCGGAGACCAG
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC
AACGGACAGTGCCAGGACCTCGCTGCTGAACTAGTGCAATTATGGCTTCTTGACAGAGGA
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCA
AGCGTGACCTTCCCAGTCCTGACGGCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACCTGAAC
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCAGCTTTCTGCAGCAGTGTGGGACCTT
GGGGTGGTGATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTGAGTTAGGGGAACCG
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG
CCTGAACTCAGGTGTACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCTTGGTCCTGCTCA
GACCAGTCTGATCCCTTGACAGACCTGCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT
GAGACCAGGACCTGTGTCTCCTCCCAAGCCCTTGGGAAGGATCTTTCTATTTCATCATCCC
TCTGGCCTAGGGGCTCAGGGGTGAGGCATCCTCCACATTCCTCCCTGGGGAAAGTTGTGT
GTTTGAGTTGAGGATGTGGGTTCTTGCTCCCTCTTTCTCCCCAGCCCAACTTGTCTCTT
TCTTACTGGTTTCAAAGTCTGATGAACGCTTCCCCTCAGAGCCACCTGGTTTCCTTGG
TTCTTGAACCTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTTAAATGCATAT
ATAAATGTAATGCAGTCACGGTCCCTTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCCAGTGG
TTTGAGACGACACACACACACACACACACACACACAGAGAGAGAGAGAGATTCTGTA
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCCTTTCTGGAAG
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCTCTCAGCTTCTAGAGG

77/113

FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT
CTTTGTCCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCCTTCTCAGGGTCTATAGATGAAC
CACACCTGCGCAGTTCCTTCTGCTGTCATCCTGGGCTTTGGTGCTTGAGAACAGCCGTG
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA
AATAAAACAGATTTGTTCATGGGACATCTAATAAATTAAATGAACTCTG

SEQ ID NO: 63_NEK7_H, N34132_H

CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGCGCCGCGAG
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCTCTCGCCGCGGCTCCTGCCCCCAAGA
ACGGCTCCAGCTCCGATTCTCTCCGTGGGGGAGAACTGGGAGCCGCGGCCCGCCGACGCTG
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCCGCCACACTATGGACAAGGACAGCCGTG
GGCGGCGCGGACCACTACCACCACTGAGCACCGCTTCTTCCGCCGGAGCGTCATCTGCG
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCTTCTCTTTCCCTGCCCCAGCCCAGCA
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG
CCACCGCCACTTCCCAGGTAGCCCAGCAGCCTCCAGCCGCTGCCGCCCCCTGGGGAACAGG
CCGTGCGGGGCCCTGCCCCCTCGACTGTCCCCAGCAGTACCAGCAAAGACCGCCAGTGT
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCCGCGCGGAGAACTGGCAGCGGCG
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTCTCTCAAGTTTGACATCGAAA
TCGGCAGAGGCTCCTTTAAGACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAG
TCGCTTGGTGTGAAGTGCAGGATCGAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG
AAGAAGCTGAAATGTTAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCCT
GGGAATCCACAGTAAAGGAAAGAGTGCATTGTTTTGGTGAAGTGAAGTATGACGTCTG
GAACACTTAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT
GGTGCCGTGAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG
GAGACCTCGGTCTGGCAACCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC
CAGAGTTCATGGCCCTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA
ATGCTGCGCAGATCTACCGTTCGCGTGACCAGTGGGGTGAAGCCAGCCAGTTTTGACAAAG
TAGCAATTCCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA
GATATTCCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG
AAGATATTAAGAAATTAAAGGGAAAAATACAAAGATAATGAAGCTATTGAGTTTTGTTTTG
ATTTAGAGAGAGATGTCCAGAAAGATGTTGCACAAGAAATGGTAGAGTCTGGGTATGTCT
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAACAAAAAGCAGGAAGAGA
GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCAGACAGGAATCAAGCAGCTCC
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG
TAGAACCTGAAGAACCTGAGGCAGATCAACATCAACAACCTACAGTACCAGCAACCCAGTA
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTCACAGAAT
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCCAANNCATGAACAGGCACATT
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG
GGGTATATCCACCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCCTCCTCAACAGA
CAGTGCAGTATTCACTTTCACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG
TGAGTCAGCCTCAAGCTCCACAAGTCTTGCTTCAAGTATCAGCTGGAAAACAGAGTACTC
AGGGAGTCTCTCAGGTTGCTCCTGCAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTCAGATGTTGCTTCAGGTATGA
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

FIGURE 2YY

GGCATTACCGAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAAT
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC
ATAATAGGAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGATCGTTTGTGGATC
AAGTGCGAGAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTCAGTGTGGAAC
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTCAGGTT
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA
TAGGCATTCCCTACCAGTTCTTTAACTCAAGTTGTTTATTCTGCGGGAAGGCGGTTTATAG
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAGTTTTCCCCAGTGAAATAACAG
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT
CCCTTAGTCTACAACAGGCCTTTTCTGAACTTAGACGTGCCCAAATGACAGAAGGACCCA
ATACAGCACCTCCAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACTTCAGGTGGTCTCCCA
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTCAAGTATCACAATACCTG
CAGTTGTCTCAATATCTACTACATCCCCGTCACTTCAAGTCCCCACATCCACATCTGAGA
TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG
CAGGGGGCAGTACTGCTACCCCAGGTCTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCACTTCATTCCCAA
GCACAGCTTCACAGCTGTCCATTAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG
AAACCGTGGTAGTTAGCGCACACTCACTAGATAAGACATCTCATAGCAGTACAACCTGGAT
TGGCTTTCTCCCTCTCTGCACCATCTTCTCTTCTCTCTCTGGAGCAGGAGTGTCTAGTT
ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTCAATTCATCAGTGATAGCTTCTACTC
CTATTCTTCCCAAGCAGCAGGACCTACTTCTACACCTTTATTACCCCAAGTACCTAGTA
TCCCACCTTGGTACAGCCTGTTGCCAATGTGCTGTGTACAGCAGACACTAATTCATA
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCCTGAAGTAGATT
CTGATACACAACCCAAAGCTCCTGGAATTGATGACATAAAGACTCTAGAAGAAAAGCTGC
GGTCTCTGTTTCAGTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA
CCTCACTAGTCATAGAGAGCACTGTACACCAGGCATCCCAACTACTGCTGTTGCACCAA
GCAAACCTCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCCTAGGAA
CAGTTGCTTTGCCAGTTACACCAGTGGTCACACCTGGGCAAGTTTCTACCCCAGTCAGCA
CTACTACATCAGGAGTGAAACCTGGAAGTGTCTCCCTCCAAGCCACCTCTAACTAAGGCTC
CGGTGCTGCCAGTGGGTAAGTGAACCTCCAGCAGGTACTCTACCCAGCGAGCAGCTGCCAC
CTTTTCCAGGACCTTCTCTAACCAGTCCCAGCAACCTCTAGAGGATCTTGATGCTCAAT
TGAGAAGAACACTTAGTCCAGAGATGATCACAGTGACTTCTGCGGTTGGTCTGTGTCCA
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTCTTCTCAAG
TCAAAGAAGGCCCTGTCTAGCAACTAGTTTCAGGAGCTGGTGTCTTTTAAGATGGGACGAT
TTCAGGTTTCTGTTGCAGCAGACGGTGCCAGAAAGAGGGTAAAAATAAGTCAGAAGATG
CAAAGTCTGTTCAATTTTGAATCCAGCACCTCAGAGTCTCAGTGCTATCAAGTAGTAGTC
CAGAGAGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG
ATGTGCCAGAGAGTGCCCAAAAATACTGCCTCAGAGGCAAAGTCAGACACTGGGCAGC
CTACCAAGGTTGGACGTTTTTCAGGTGACAACTACAGCAAACAAAGTGGGTCTGTTTCTCTG
TATCAAAAATACTGAGGACAAGATCACTGACACAAAGAAAGAGGACCAGTGGCATCTCCTC
CTTTTATGGATTTGGAACAAGCTGTTCTTCTGCTGTGATACCAAAGAAAGAGAAGCCTG
AACTGTACAGAGCCTTACATCTAAATGGGCCGTCTTCTGACCCGGAGGCCGCTTTTTTAA
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA
GCCTTCTTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTTAACTCCTCTTACATGA
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC
GAGATAAACATCTCAAAGAGATTACAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

FIGURE 2ZZ

CTTTGTATACCAAACCTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC
TTTCAGGGAGAAAGACGACGACCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT
CCTTGGGGGAATAAAAGCCCCCAGCTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG
TCTTGCACCCCCAGCAGACCCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC
AGCTGTTACAGCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTTCAGCCTTCACCA
GTGATGGTGGCATTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTAAAG
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACACTGAAGAATCTGG
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC
TCATTTGGGATTTGGAACCTTAGGCTTTAATATTAGGCTGAGATTTCTGGAATGAAATTCT
AAGGTGTTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTACAGTTTTTTATCCA
TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATTTCCACAGAG
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA
GATCAGTCTCTTCACAGGAAGAATGCACCTTGATTGGTAAGGAGGGCAAACCTAGCTAGCAT
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT
CATCTCTTACATATCTGACCTTCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG
CATTTACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC
TCTCTGTGTTCTACCTGTTTTTCCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT
GGCTCTTTGTGTGTAACACCTTTACTCCTTCTTGTCTTGTGTTTCTGCTGCTTGGATC
TGATGTTTTCACGCAGTCCATTTTTCATTTGTCTCTTTTTGTATATCATCTACTCAGTGGCT
TGGCTGAATTACTGTTACCTCAGAAGTTTGGGCCCCCACATTAATTATGATAAAAAATG
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACCTTCTGGTAGAAGTGCTTCTTCAT
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCAATTTAGAAT
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA
GGCGGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC
CCATCTCT

SEQ ID NO: 64_BCON3_H

GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT
GAAGCGCAGGCTGCGGGGCGCGGAGTCGGGAGGCCTGAGTGTTCTTCCAGCATGTCCGA
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC
AGCTCCTGGCCTGACATCAGTGTCACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAAGAGTCGCCCTGTGGGCG
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTGTGTGGAATGAGGTACAGTTCTCTGA
ACGCAAGAATAACAAGCTGCAGGAGGAAAAGGTTCTGTGCTGTGTTTGATAATCTGATTCA
ATTGGAGCATCTTAACATTGTAAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAA
GGCCAGGGTCATTTTTATCACAGAATACATGTCTGAGTCTGAAGCAATTTCTGAA
GAAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACA
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCT
GACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTGGCTCC
TGACACTATCAACAATCATGTGAAGACTTGTGAGAAGAGCAGAAGAATCTACACTTCTT
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTACGGGCAATGGAGAGTCCTCATATGT
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGT
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACCTCCTTGCGGCCCACTGCATTGTGGG
ACACCAACACATGATCCAGAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAG
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC
TCAGTCACCAGCTCTGGAATTAGATAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC
ACTTCTGCTGAAGTTGGAGGACAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA
CAGTACCCTCAACTCAGCCGCTGTACCGTCTCCTCTTAGAGCTCACTCGGGCCAGGCCC
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC
AGTATTACCCTGTGAAGCCCCCTCCCTCCTTTATTATTACAGGAGGGCTGGGGGGGCTCCC
TGGTTCTGAGCATCATCCTTCCCCCTCCCCCTCTCTCCTCCCCCTCTGCACTTTGTTTACT
TGTTTTGCACAGACGTGGGCTGGGCTTCTCAGCAGCCGCCTTCTAGTTGGGGGCTAGT
CGCTGATCTGCCGGCTCCCCGCCAGCCTGTGTGGAAGGAGGCCACGGGCACTAGGGGA
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGGAGAGAAAGGTGGTGCTGCAGTG
GTGGCCCTGGGGGGGCCATTGATTGCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT
GCT

SEQ ID NO: 65_AA711829_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG
AAACGCTGGTGTACACAGATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCTCCC
ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAAACGGACTCATCAAG
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTCAGGGCAAT
GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC
TCATTACAGAGGGAGTTTATTCAAAGTGCTGCAGTCTGAGCCTGCTCGGAGACCAACA
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT
GCTCACTGTATCGTGGGGCACCAACACATGATCCAGAGAACGCTCTAGAGGAGATCACC
AAGAACATGGATAACAGTGCTGTACTAGCTGAAATTCCCGCAGGGCCAGGACGAGAACCA
GTTACAGACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC
AGGAATGGGATCTACCCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCCTGAGCCAGCT
GAAGTGAGACACGAAAGGTGGTGCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC
TTCATTAGTGAGGCTGATCAGAGCCGCCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTCACCGTCTCCTCGTAGAGC
TCACTTGAGCCAGGCCCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCCTCCT
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATTATTATTAGGAGGGCTTTAGGG
GCTCCCTGGTTGAGTATCACCTGCCCTTCCCCTCTCTTCTCCTCCCCCTCTGCACTTTGTT
TACTTGTTTTGCACAGACGTGGGCTGGGCTTCTCAGCAGCCACCTTCTAGCTGGGGGC
TAGTAGCTGACCTGCTGCCTCCTGCCCTACTTGTGTGGACAGGAGGCCACGGGCACTGG
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA
GGGGTGGCCCCCGGGGGGGGCATTGCAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC
TTTTTGCT

81/113

FIGURE 2BBB

SEQ ID NO: 66_AA099102_H

ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCTC
TCATCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTCACCGAGTGTGAGCCG
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCTGGAGGCCGATGGCCAAGAG
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCCCACCTCTCCGGTCGCAAGCTGTCT
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC
TGCATCTGCCCGTCCCTGCCCTACTCACCCGTCAGCTCCCCGCAGTCCTCGCCTCGGCTG
CCCCGGCGGGCCGACAGTGGAGTCTCACACGTCTCCATCACGGGTATGCAGGACTGTGTG
CAGCTGAATCAGTATACCTGAAGGATGAAATTGGAAAGGGCTCCTATGGTGTCTCAAG
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG
CTGATCCGGCAGGCCGCTTTTCCACGTGCGCCTCCACCCCGAGGCACCCGGCCAGCTCCT
GGAGGCTGCATCCAGCCCAGGGGCCCATTTGAGCAGGTGTACCAGGAAATTGCCATCCTC
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCTGGATGACCCCAATGAG
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCCAAC
CTCAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT
GACGCGCTCCTCTCCAACCTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA
TACTGCTTTGTCTTTGGCCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGT
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGCTGCCGGAAATC
AAGCTGCACCCCTGGGTACGAGGCATGGGGCGGAGCCGTTGCCGTCCGAGGATGAGAAC
TGCACGCTGGTTCGAAGTGACTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTCAGCGCCTGGAACTTGCTCACCAAAAAA
CCAACCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT
CCAGGGCACCGACCCGCCCGCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC
TGCGTGGAAAGTTGCTGGGCCCCCGCCCCGGCTCCCCCGCACGCATGCATCCACTGCGG
CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67_5R69_17_2_H

CCGGGATGTGAGCCTGGTGGTTGGCAGCTGGAGCCACGTCCGAGGGGGGAAGTGTGCGCAGC
ATTCTCTGCAGGCATCACAGACCTGAGGCAGTGGCCTCCGGAGGGGCACTGGACAGAAACA
GCCATCCAAGTGCTGAGTGGAGGGACCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT
CCCTCAGGTAGGGATCGGGGCGCCTTGTCGCCGCCAGCCACGTGTGGCGTCCGGTACAGT
CAGCAGAGTGCAGGGTGCGGGCACCAAGAAAGGGGGCGCAGGGGAACTCCCGCGGGCCTC
GCGTTTGCAAACCTTCTCGCCTGGGCAGGAGGCGGTCTGGGAAAGAAGGTGGAAGAGCGA
GCTTTTGGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA
TGGAATAATTTGAAGCATATTATCACCCCTTGCCAGGTTCATCCACAAACGGTGTGAAGAGA
TGAAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCCTCGGCCTGATCAAGC
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTTCAGCA
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG
TGAACAGGAAGCTGAGTGATGTCTGGAAGGAGCTCTCGCTGTTACTTCAGGTTGAGCAAC
GCATGCCTGTTTCAACCATAAGCCAAGGAGCGTCCTGGGCACAGGAAGATCAGCAGGATG
CAGACGAAGACAGGCGAGCTTTCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAAACTTTGAGGCAGTGTAAGT
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAACCTAGAAGTCATCAGTTTACTGGGAC

82/113

FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC
CACAGGTTTGGGGATCCATTCATGGCTAGCCCAGGCTTCTGTCCATGGAATAACATGTGG
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT
ATGAATAGAATCAAAGCTTCAGTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAAA
TTTAAATGCCCACTCATTTCATTTCATCAACAAAACCTGTGAGTATCTGGTTTATGCCAGA
GGCCATGCAAAGAGGTAACTAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC
CAAGCTCTGGGTAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG
GGTTAAGGCTGGAGGGACAGGCGGGATTTGAAGAGGAGGAAAGGAAGTGGATGACACAT
TCTGTAACTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT
GGGCTGAGTCCATCAGAAGCCCCAGCCACCACAGCTCTGGTTCATGTAGTAGAGCTTCC
CACTCACACATCACAAATATGCCACCTCCCTTAGGACCCCTTCCCTCTGCTCATTGACTCT
TTTGTCTTCTTCCCTCTCGGGGGTGAGGTGAGATTTACCACCAAAATGCATGCAGGAGAT
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATAACCACAGAGCTCCAGTGGC
CATAAAAGTATTCAAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA
TAAGGAGATCAAAACCATGAAGAAATTCGAATCTCCCAACATCCTGCGTATATTTGGGAT
TTGCATTGATGAAACAGTGACTCCGCCTCAATTCTCCATTGTTCATGGAGTACTGTGAACT
CGGGACCCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGCAAGCGCATGGT
CCTAGTCCTGGGGGAGCCCGAGGCCTATACCGGCTACACCATTGAGAAGCACCTGAACT
CCACGGAAAAATCAGAAGCTCAAACCTTCCCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC
AGGATTTGAGTTGAGGAAAACACAGACTTCCATGAGTTTGGGAACTACGAGAGAAAAGAC
AGACAGAGTCAAATCTACAGCATATCTCTCACCTCAGGAACTGGAAGATGTATTTTATCA
ATATGATGTAAAGTCTGAAATATACAGCTTTGGAATCGTCCTCTGGGAAATCGCCACTGG
AGATATCCCGTTTCAAGGTGAAGAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTCTG
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGCCCCATGATCCCTCTGTGCGGCCCT
CTGTGGATGAAATCTTAAAGAACTCTCCACCTTTTCTAAGTAGTGTATCAAAATCTAAA
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAACTGGACATCTCTCTCTCAT
ATCCTTCGGCATTGGGTTATCTATGGGTGCAAGGAGTGGGCACGCTTCTCTGTTACAAAT
AGAAAACGATTCCAGTCATACAGGACACATCCCACTCCAAATGATATTTCCAAAAACATA
CCTCTGACAGTAACTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT
CTTGGCAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATT
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGACTGTAT
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA
TCAAGACCAGAAGAACCACTCAAGCAGATCCCAGCCCAAATTGCCCATTCACACAATCAG
GAGCTAAATAAATTACTGTTGTCTTTT

SEQ ID NO: 68_H85811_H

CGCCCCGGCCCCCTCCCCCGGCGCCGGCCACGGGAGGCGGTGATGCGGGCGCGGGCGGCCT
CGGCTGCGCCGAGAGCGGAGACACAGGCTCAAGATGGCAGATTCGCACTGAGGCTGGGGG
GGCCGAGCTCGCGCGCCGCTTTCCCGTCCCCGTTGCCATGAACCGCGGACACCCCGGCCC
CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTTCTCCCCTCACACCC
TTCAATCAAGTGCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAACTGGG
ACATGACTGGGTACGGCTCCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCCAAGCCTACCTT
ACGAGCAGACCATCGTCTTCCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

FIGURE 2DDD

GCACTTCTGTCACCGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTCTGAAGCACTG
TGAGCCTCCTTGATACCTACCAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTGAGAATAATGCAAGCG
GGGCCACTGTGCGCCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG
AGGTCTTAGAGTTCTTGGGCCGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAAACGGG
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCCGACAAG
GTCAGATTGAAGTGAGCATCCTGGCCCCGTTGAGCACGGAGAGTGCCGATGACTATAACT
TCGTCCGGGCCCTACGAATGCTTCCAGCACAGAACCACACGTGCTTGGTCTTCGAGATGT
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCCTTGCCCCCTCAAAT
ACATTGCCCCAGTTCTCCAGCAGGTAGCCACAGCCCTGATGAAACTCAAAGCCTAGGTC
TTATCCACGCTGACCTCAAACCAGAGAACATCATGCTGGTGGATCCATCTAGACAACCAT
ACAGAGTCAAGGTCATCGACTTTGGTTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA
CCTACTTGCAGTCCAGATATTACAGGGCCCCCTGAGATCATCCTTGGTTTACCATTTTGTG
AGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGCAGAATTGTTTCTGGGTTGGCCGT
TATATCCAGGAGATTCGGAGTATGATCAGATTGCGGTATATTTACAAAACACAGGGTTTGC
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACCTAGGTTTTTCAACCGTGACACGG
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA
TTAAGTCAAAAGAAGCAAGAAAGTACATTTTCAACTGTTTAGATGATATGGCCCAGGTGA
ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGGCGGGAGT
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG
AAACCCCTGAACCATCCCTTTGTACCATGACACACTTACTCGATTTTCCCCACAGCACAC
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC
TGACCATGACCTTTAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA
TGGCTGCAGTGGCCCAGCGGAGCATGCCCCTGCAGACAGGAACAGCCCAGATTTGTGCCC
GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAGG
CCTCTCCCTCTAAGCACGCTGGCTACTCGGTGCGAATGGAAAATGCAGTTCCCATCGTCA
CTCAAGCCCCAGGAGCTCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCCAGCAGGCTT
GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC
AGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGC
AGCCTGCACTATTGACCGGTCATGTGACCCTTCCAGCAGCACAGCCCTTAAATGTGGGTG
TGGCCCACGTGATGCGGCAGCAGCCAACCAGCACCCTCCTCCCGGAAGAGTAAGCAGC
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCCTCTCAGGCCATCAGCT
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTGTGCCATGGTGCACA
GTAGCCCGGCCTGCAGCACCTCGGTCACTGTGGGTGGGGCGACGTGGCCTCCAGCACCA
CCCGGGAACGGCAGCGGCAGACAATTGTCATTCCCGACACTCCCAGCCCCACGGTCAGCG
TCATCACCATCAGCAGTGACACGGACGAGGAGGAGGAACAGAAACACGCCCCCACCAGCA
CTGTCTCCAAGCAAAGAAAAACGTATCAGCTGTGTACAGTCCACGACTCCCCCTACT
CCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG
TGCCAGTCAACACCAGTCAACACTCGTCTCTTACAAGTCCAAGTCTTCCAGCAACGTGA
CCTCCACCAGCGGTCACTCTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCCACCATGG
CCCAGGCTCCGTACTCCTTCCCGCACAAACAGCCCCAGCCACGGCACTGTGCACCCGCATC
TGGCTGCAGCCGCTGCCGCTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCACCTGGTGGCCTCGCAAGGCTCTG

FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA
GCATGGGCCCCCGGGTCTGCCCTCGCCCAACCATCCACCCGAGTCAGTATCCAGCCCAAT
TTGCCCCACCAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCCAC
TGAGCCCCGCCAAGGTCAACCAGTACCCTTACATATAAACACTGGAGGGGAGGGAGGGAG
GGAGGGAGGGAGAGAATGGCCCCGAGGGAGGAGGGAGAGAAGGAGGGAGGCGCTCCTGGGA
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG
GGCGGGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTCTGGGACACCAGTGAACTTGAACC
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTTTAAAGGAAGGGATTAAAGAG
GGTGGGAAATCTATGGTTTTTTATTTTAAAAAAG

SEQ ID NO: 69_DYRK3_H

CGGGAGCGAAAGTGCCTGAGCTGCAGTGTCTGGTTCGAGAGTACCCGTGGGAGCGTCGCG
CCGCGGAGGCAGCCGTCCCGGCGTAGGTGGCGTGGCCGACCGGACCCCCAACTGGCGCCT
CTCCCCGAGCGGGGTCCCGAGCTAGGAGATGGGAGGCACAGCTCGTGGGCCTGGGCGGAA
GGATGCGGGGCCCGCTGGGGCCGGGCTCCCGCCCCAGCAGCGGAGTTGGGGGATGGTGTC
TATGACACCTTCATGATGATAGATGAAACCAAATGTCCCCCTGTTCAAATGTACTCTGC
AATCCTTCTGAACCACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA
GATCATACTCAGCACTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA
TTTGGCAACAGAAAATCCAATACTATTCACTCAGATGGCATCAGTGAATCTGAAAAATGC
TCTCCTACTGTTTCTCAGGGTAAAAGTTCAGATTGCTTGAATACAGTAAAATCCAACAGT
TCATCCAAGGCACCCAAAGTGGTGCCTCTGACTCCAGAACAAAGCCCTGAAGCAATATAAA
CACCACCTCACTGCCTATGAGAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTA
GGTCCAAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT
GATGCAGATGGGGCCTATATTTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG
CTGAAAATTATTGGCAAGGGGAGTTTTTGGGCAGGTGGCCAGGGTCTATGATCACAACTT
CGACAGTACGTGGCCCTAAAAATGGTGCGCAATGAGAAGCGCTTTCATCGTCAAGCAGCT
GAGGAGATCCGGATTTTGGAGCATCTTAAGAAACAGGATAAACTGGTAGTATGAACGTT
ATCCACATGCTGGAAAGTTTCACATTCCGGAACCATGTTTGCATGGCCTTTGAATTGCTG
AGCATAGACCTTTATGAGCTGATTAAAAAAATAAGTTTCAGGGTTTTAGCGTCCAGTTG
GTACGCAAGTTTGGCCAGTCCATCTTGCAATCTTTGGATGCCCTCCACAAAAATAAGATT
ATTCACCTGCGATCTGAAGCCAGAAAACATTCTCTGAAACACCACGGGCGCAGTTCAACC
AAGGTCATTGACTTTGGGTCCAGCTGTTTTCAGTACCAGAAGCTCTACACATATATCCAG
TCTCGGTTCTACAGAGCTCCAGAAATCATCTTAGGAAGCCGCTACAGCACACCAATTGAC
ATATGGAGTTTTTCGCTGCATCCTTGCAGAACTTTTAACAGGACAGCCTCTCTTCCCTGGA
GAGGATGAAGGAGACCAGTTGGCCTGCATGATGGAGCTTCTAGGGATGCCACCACCAAAA
CTTCTGGAGCAATCCAAACGTGCCAAGTACTTTATTAATTCCAAGGGCATAACCCCGCTAC
TGCTCTGTGACTACCCAGGCAGATGGGAGGGTTGTGCTTGTGGGGGGTTCGCTCACGTAGG
GGTAAAAAGCGGGGTCCCCCAGGCAGCAAAGACTGGGGGACAGCACTGAAAGGGTGTGAT
GACTACTTGTTTATAGAGTTCTTGAAAAGGTGTCTTCACTGGGACCCCTCTGCCCGCTTG
ACCCAGCTCAAGCATTAAGACACCCTTGGATTAGCAAGTCTGTCCCAGACCTCTCACC
ACCATAGACAAGGTGTCAGGGAAACGGGTAGTTAATCCTGCAAGTGCTTTCCAGGGATTG
GGTTCTAAGCTGCCTCCAGTTGTTGGAATAGCCAATAAGCTTAAAGCTAACTTAATGTCA
GAAACCAATGGTAGTATACCCCTATGCAGTGTATTGCCAAAACCTGATTAGCTAGTGGACA
GAGATATGCCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAAATGGA
AAAAATGCAAGCCCATTGGTGGATGTTTTTGTAGAGTAGACTTTTTTTTAAACAAGACAA
AACATTTTTATATGATTATAAAGAATTCTTCAAGGGCTAATTACCTAACCAAGCTTGTAT
TGCCCATCTGGAATATGCATTAAATGACTTTTTTATAGGTCA

85/113

FIGURE 2FFF

SEQ ID NO: 70_AA589241_M DYRK3_M

CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAACTTCTGGAGCAATCCAAGCGTG
CCAAGTACTTTTATTAACCTCAAAGGCTTGCCTCGATACTGCTCCGTATCTACCCAGACGG
ACGGGAGGGTGGTGCTTCTCGGGGGTCTGCTCACGCAGGGGTAAAAAGCGAGGCCCGCCAG
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTCATAGAGTTTC
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCCGCTCACCCCGGCTCAAGCATTAAAGAC
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC
GGGTAGTTAACCCTACAAATGCTTTCCAGGGACTGGGTTCGAAGCTGCCTCCAGTCGTTG
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT
GTATTTTTTAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTCAC
TGATGGATATGTTTTTGTAGACTTTTTTTTAAACAAGGCAGAACATTTTTATATGACTAT
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71_5R72_16_2_H

GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGA
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA
CGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCAGGACCGGTCAAAGAGCCCCCTGA
AATCAATTTAGTTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA
TTTGAGGGTTAAATGCCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAA
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGC
CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA
AATCCTGCATGAGATTGAGAGAAGGAAAGAAGAGATAAAAAGAAGAGAAAAAAGGAAAGA
AATGGCTAAGCAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACTCTAA
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT
AGGAAATGGTAAACATCGGGCAAACCTCCTCAGGAAGGTCTAGGCGAGAACGTGAGTATTC
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAG
TCCTGATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACCTTGGA
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTGTATGAGTGGGT
CCTTCAGTGGCAGAAAAAAATGGGTCCATTCCCTTACCAGTCAAGAAAAAGAGAAGATTGA
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAG
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTGAGGCCTTGA
TTATCTGCACAGCAATTCTGTGGTGCATAAGGTCTTGAGTGCATCTAATGTCTTGGTGGA
TGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG
CAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAA
AACGGGGAAGAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGA
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT
GAAACACAGCTTTATAAATCCCCAGCCAAAATGCCTCTAGTGGAACAAAGTCCTGAAGA
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC
CTTCTTTTAGTGAGACACAGAGACAGTTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTG
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCGCGAGGATCAA
GGGCGAAGTGACACTGCTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC
CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC

FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA
CAGCGTAGAGGCCGCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC
GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGA
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCAGTCCTTCCTGCCTGCTTCAGA
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA
TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC
TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCAT
TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTTCGAGAGATTCTGGA
TGGATTAGCTTATATCCATGAGAAAGGAATGATTACCCGGGATTTGAAGCCTGTCAACAT
TTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTTGGCGACAGACCATCT
AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC
TTCAGGTCACCTTAAGTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG
AAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTT
TGAGATGTCTTATCACCCTATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT
CAGAGATCCCCTTCCGCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA
GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAAACGGCCACAGCCACAGA
GCTGCTCAAGAGTGAGCTGCTGCCCCCACCACAGATGGAGGAGTCAGAGCTGCATGAAGT
GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCCAGAT
CTTCTCGCAGCGCATCTCCCCTGCCATCGATTACACCTATGACAGCGACATACTGAAGGG
CAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCAT
CTTTAAAGACATGGAGCTGTTTCAAGTTGTGTACTCCACTACTGCTTCCCCGAAACAGACA
AATATATGAGCACAACGAAGCTGCCCTATTATGAGACCACAGCGGGATGCTGGTGATGCT
TCCTTTTGACCTGCGGATCCCTTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTT
AAAACGATACTGCATAGAACGTGTGTTTCAAGCCGCGCAAGTTAGATCGATTTTCATCCCAA
AGAAGTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCCCAC
TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG
AAATTACAGTATTTATTTGAACCATAACCATGTTATTGAAAGCAATACTCTTACACTGTGG
GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA
GCTGACGAGGAGAGAAGTGGAAAGCTAAATTTTGAATCTGTCTTTGTCTTCTAATAGTCT
GTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTGCAAGATCTTATGCCAACAAT
AAATTATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGA
CCTAGAGGAGGTTGTTGGACTGTTGAAGAACTCGGCATCAAGTTACAGGTCTTGATCAA
TTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT
CATCAAACGAAGGCCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT
GCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCCTGCCATTGGGGT
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCTCAACATGGAGGAATCTGTTACAAT
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTGTCAGATGTCTATGTCCAGGGCCATCAA
CCTAACCAGAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACA
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAAGGCAGACAGA
GAAGCGTGTGCTGGAGACTGAACCTGTGGACCATGTACTGCAGAACTGAGGACTAAAGT
CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATCTGAAGGG
GTCATTTTCTAATGCTTCAAGTTTGTGTTGAAATCCATGGAGCAACAGTGGTTCCCATTGT
GAGTGTGCTAGCCCCGGAGAAGCTGTGAGCCAGCACTAGGAGGCGCTATGAAACTCAGGT
ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAAT
TCTGGCTGTGGATCTACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGC
TGATGAACAGGCATTTAACACAACCTGTGAAGCAGCTGCTGTACGCCTGCCAAAGCAAAG
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGT
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAAC
TGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT

FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA
TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG
CCT

SEQ ID NO: 73_R43524_H, HRI_H

ATGCTGGGGGGCAACTCCGGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCT
GTGGCTGCGCCGCCGCCATCGACTTTCCCGCCGAGGGCCCGGACCCCGAATATGACGAA
TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCCTACAACAGCCAACCTTCCCT
TTTGCAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT
GAACCAAACCCACTTCGTTCAAGACAGGTGTTTAAAGCTACTTTGCCAGACGTTTATCAAA
ATGGGGCTGTTGTCTTCTTTCACTTGTTAGTGACGAGTTTAGCTCATTGAGACTACATCAC
AACAGAGCTATTACACACTTAATGAGGTCTGCTAAAGAGAGAGTTCGTCAGGATCCTTGT
GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAACT
TCACGTTACTTAAATGAATTTGAAGAACTTGTCATCTTAGGAAAAGGTGGATACGGAAGA
GTATACAAGGTGAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATT
AAGGGTGCAACTAAACAGTTTGCATGAAGGTCTACGGGAAGTGAAGGTGCTGGCAGGT
CTTCAGCACCCCAATATTGTTGGCTATCACACCGCGTGGATAGAACATGTTTCATGTGATT
CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG
GAAGAGGACAGAGAGCAATGTGGTGTAAAAATGATGAAAGTAGCAGCTCATCCATTATC
TTTGCTGAGCCCACCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAAATCAG
AATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACCTTGAG
TCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTGTGTCTGCCAGTTCAATTGTGGAA
CAGCAGCTGCCACTCAGGCGTAATTTCCACCTAGAGGAGAGTTTCACATCCACCGAAGAA
TCTTCCGAAGAAAATGTCAACTTTTTTGGGTGACAGAGGCACAGTACCACCTGATGCTG
CACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAG
CGGGGCCGGGAGTATGTGGACGAGTCTGCCTGTCCTTATGTTATGGCCAATGTTGCAACA
AAAATTTTTCAAGAATTGGTAGAAGGTGTGTTTTACATACATAACATGGGAATTGTGCAC
CGAGATCTGAAGCCAAGAAATATTTTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGA
GACTTTGGTCTGGCCTGCACAGACATCCTACAGAAGAACACAGACTGGACCAACAGAAAC
GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGTTTCACCCGAA
CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCTGT
CTAGAGCTCTTTCAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAGTTCTAACAGGTTTA
AGAACTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC
CAGCACTTAACGAGAAGGAACCTCATCGCAGAGACCATCTGCCATTGAGCTGCTGCAGAGT
GAACTTTTCCAAAATTCTGGAAATGTTAACCTCACCTACAGATGAAGATAATAGAGCAA
GAAAAAGAAATTGCAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTG
AGGGATGACGGAAAGGATGGGGGCGTGGGATGA

SEQ ID NO: 74_17000057519457_H

CACAAGAGCCCTTCTGTCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT
AACCACCTTACAGGCCGGAAGTGTCCGGGGTGGACGCATTCGGGTAGCCGAAGAAGTCCCA
GGATTGCCGAAGAAGTCCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAG
AGACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTA
CGCCGGCCGATGGCGAGGAGCCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCGGGAGC
GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGT
TCCGTGGCCGCTTCCAGGGCCGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACC
GGCACCCGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGC
TCCTCCGCTGTGCGCGCGCTGGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTT
CCAAGTCTTATATATGGAAGAAATTGAAGGCTCAGTGAAGTGTTCGAGATTATATTCAGT
CCACTATGGAGACTGAAAAAACTCCCCAGGGTCTCTCCAAGTTAGCCAAGACAATTGGGC

FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTCATGGTGATCTCACCACCTCCAACA
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT
TCATTTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC
TCAGTACCCATCCCAACACTGAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCT
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG
ATATTTTTTAAGTGATGTGATCGTGTCTATTATCATCTGCACTTCACTCAAGAGCTTACT
ATGTGTCTAAGTCATGTTCTAGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTT
CTCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA
GAACATTATTCTCTTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC
GCTGAGCTTACTGGCCCTCTAACCCAGTGTTTTTTTTTTGTTGTTGTTGTGTACATGTTAT
ATTTATTTTGAACACAGTTTAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA
CAGCATGGAAAATATCAGTGTATTGTTTTATGAAACTTTTACGTGTATATATAGACCAAG
GATATGTGCTGAGTTTTGATGTCAAATATATTTCTCTTTCAGGGTCATGATCAAAAAATG
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC
TGAAATTCATGTTAACATGTTTTTATTTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA
AGACAAGTGATTGATCTAAAGTTTCTTTTAAGTTTATACCGCTAAACAACTGAGTTGAT
TTCTATCACAGGCAGTAAGTAGGTAGAGCAAAAATGGTGAAGTGACTTGTGAAGACTGAA
GTTTGATGAAGTCTGGTTTAAGGCACAGGTAACTGAGTGTGGATGCAAAAGTACCAGGA
GCTAGCTTTTAACTTGCCAGCCTCAGTTTCTTTTCTTAGAAGAAGCTATGTTTGGGTG
GGAAGGGAAGAGAGGGATAAGAAAATACCTTTCTTCTTGTAACTCCAATCAACAAACA
TATTTTGAGTGCCTTTTGTGTTCTTGGCACCCTGTTGGGTATTGGGTACTTGGCACCCT
GTTGGGTATTGGGTACAATGGTGAGCCAGACAGACACAGCGCCTGTCTTTTGTAAAGAT
ATTTATTTTTTATAAAAAAGTATAAAGTATACAGTGGGATGTTTTGATATACATTATGAAA
TGATTGCTACAGCTGAGCTAATTAACACCCATCACCTCACATAGTTACTGTCTTGTCTTCT
TAATATGGACATTTGCAGCTATGAATTTCCCTCTGCACACTGTTGTCATCACACACTCTC
AGTTTTGGTATTTTGTGTTTTTGTGTTTCATTTCATCTCAAAGTATTTTCTAATTTCCCTTG
TGATTTCTTCTTTGACCCCTTGATTGTTTAGAAATCTGTTAATTTCCACACATTTGTAAA
TGTTCCAATTTTTCTTTTGTATTGTCAGCTTCATTCCATTGTGTTTCAAGATGATACAG
TCAGTGCCTGTTCTTATGAAGCAAACATTCTATAATAGTAGGACCAGTACCCTGTCTGTT
TCATTACCCACAGTCAGCATGCCCCAAGTGCCAGCATGGGGCGGATGGCCAGGAATGAG
TGAAAACTTCCCTTCTGGGTAGTTGTGACTAGTAGAGAGGAAAAATAATATAATTGCCT
GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTTATATTGGATCTAAAATAACTCTTA
AGTTAGGCATTATCCCCATTTTATAGATGGAGAACTGGCCCCAAAAGGTGGGAACCTGT
CCAAGACGTACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA
CTGACAAATGAGATATGGGATATGGTGCATCTTTACAGTACTATAATAAGTATTGGCGTA
TAACATTATTTTCAAGGAACCTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT
TCCCAACATGAATGAGATGCCTCATTCTCAGTTTCTCAGGTGTACTATAAGGCTAGTA
CCTGCTTTGTTGGGGTATGGTTGGCTCGTGTGCATTAAGTCAACAAATCCCTAGT

SEQ ID NO: 75_AA013524_M

CTGGTGCAGCAGGGCGCCGAGGCGCGGTTTTCCGTGGCCGCTTCCAGGGCCGCGCGGCC
GTGGTGAAGCACCGCTTCCCGAAGAGTTACCGGCACCCGGAGCTGGAGGCGCGGCTCGGC
CGTCGGCGGACGGTGCAGGAGGCGCGCGGCTGCTCCGCTGCCGCCGTGCGGGGATAGCT
GCCCCAGTCGTCTTCTTTGTGGACTATGCGTCTAACTGCTTATATATGGAAGAAATCGAA
GACTCGGTGACTGTTCCGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG
TGCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC
CTCATTCACGGGGACCTCACACCTCCAACATGCTCCTGAGGCGGCCCCCTGGCGCAGCTG
CACATCGTGTCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG
TTTGAAGCCTTTCTGAAGAGTTACGGGGCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGAGCTGT
GGTGAAGTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG
GGTTGTAAAGTGGTCTGTGATCGTGCTGGGCCACCACCATCCATGGCTCACTGTTCTCAG
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGGAAGAGGTTATAAGCCACCATACCT
GACTTTGCACTGATTCTGTCAGAAAC

SEQ ID NO: 76_17000139801197_H, IRAKM_H
ATGGCGGGGAAGTGTGGGGCCCGCGCGCTGTGCGGCACACGCTGCTGTTTCGACCTG
CCGCCCCGCGCTGCTCGGAGAGCTCTGCGCTGTTCTGGACAGCTGCGACGGCGCGCTGGGC
TGGCGCGGCCTGGCAGAGAGACTTTCAAGCAGCTGGCTGGATGTTTCGTCATATTGAAAAG
TATGTAGACCAAGGTAAAGTGAACAAGAGAATTACTTTGGTCCTGGGCACAGAAAAAC
AAGACCATCGGTGACCTTTTACAGGTCCTCCAGGAGATGGGACATCGTCGAGCTATTCAT
TTAATTACAACTATGGAGCAGTGTTGAGTCCTTCAGAGAAGAGTTATCAGGAAGGTGGA
TTTCCAAATATATTATTCAAGGAAACAGCCAATGTCACCGTGGATAATGTTCTTATTCCT
GAACATAATGAAAAAGGAGTACTGCTTAAATCTTCCATCAGCTTTCAAAATATCATAGAA
GGAAGTAGAAATTTCCACAAAGACTTCCTAATTGGAGAAGGAGAGATTTTTGAGGTATAC
AGAGTGGAGATTCAAAACCTAACATATGCTGTCAAATTATTTAAACAGGAGAAAAAATG
CAGTGTAAAGAAGCATTTGGAAGAGGTTTTTATCTGAGCTTGAAGTTTTACTACTGTTTCAT
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT
TATCCATACATGAGAAATGGAACACTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCC
CCACTCCCTTGGCACATTTCGAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC
CTGCACAACGTTCAACCATGCTCGGTTCATCTGTGGCAGTATATCAAGTGCAAACATCCTT
TTGGATGATCAGTTTCAACCCAACTAACTGATTTTGCCATGGCACACTTCCGGTCCCAC
CTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTAC
ATGCCAGAAGAGTACATCAGACAGGGGAACTTTCCATTAAACAGATGTCTACAGCTTT
GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTTAGATGATCCAAACAT
ATCCAGCTGCGGGATCTCCTTAGAGAATTGATGGAGAAGAGAGGCCTGGATTTCATGTCTC
TCATTTCTAGATAAGAAAGTGCCTCCCTGCCCTCGGAATTTCTCTGCCAAGCTCTTCTGT
TTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTTA
AATACTCTTGAAAGTACTCAAGCCAGCTTGTATTTTGCTGAAGATCCTCCACATCACTA
AAGTCCTTCAGGTGTCCTTCTCCTCTATTCTGGAGAATGTACCAAGTATTCCAGTGGA
GATGATGAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCCTGAGGATAGACAGA
ATGACTCAGAAAACCTCTTTTGAATGCAGCCAGTCTGAGGTTATGTTTCTGAGCTTGGAC
AAAAAGCCAGAGAGCAAGAGAAATGAGGAAGCTTGCAACATGCCAGTTCTTCTTGTGAA
GAAAGTTGGTTCCCAAAGTATATAGTTCCATCCCAGGACTTAAGGCCCTATAAGGTAAAT
ATAGATCCTTCTTCAGAAGCTCCAGGGCATTCTTGCAAGAGCAGGCCAGTGAGAGCAGC
TGTTCTCCAAATTTTCTGGGATGAATATGAACAGTACAAAAAGAATAA

SEQ ID NO: 77_AA840598_M IRAKM_M
ATGTGGAAGAGATTTTTATCAGAACTGGAAGTTCTACTCCTGTTCCGTCACCCCCACATA
CTAGAGCTGGCTGCATATTTACGGAGACTGAGAACTTTGTCTGGTTTATCCCTATATG
AGCAACGGGACGCTTTTCGACAGATTACAGTGACAAATGGCACAACCCCGCTTTCCTGG
CACGTTTGAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGCACAACACT
CAGCCGTGCGCCGTCATCTGTGGCAACGTTTCCAGTGCAAACATACTCTTGGATGACCAG
CTCCAACCCAACTAACGGATTTTGCTGCAGCGCACTTCCGACCCAATCTAGAGCAGCAG
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

20/113

FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACCTGATGTCTACAGCTTCGGAATCGTGATC
ATGGAGGTTCTAACGGGCTGCAAAGTGGTGCTGGATGACCCGAAACACGTTTCAGCTGCGG
GACCTCCTCATGGAAGTCTGAGAGAAAAGAGGCCTAGACTCCTGCCTGTCTTCTTAGAC
AGGAAGATAACCACCTGTCTCGGAACCTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG
TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCTGTCTCTCTGGAG
AGCACCAGCCTAGCTTGTATTTTGCAGAAGACCCTCCACGTCCTTGAAGTCCTTCAGG
TGTCTTCTCCACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAAC
CAGAATAACCATTTCAGTACCTCCCAAGGAAGTTTGGGGACAGATAGAGTGAAGTTCAGAAA
ACCCCTTTGAATGCAGCCAGTCTGAGGTACCTTTCTAGGCTTGGACCGAAACAGAGGG
AACAGGGGAAGTGAAGCGGATTGCAACGTGCCAGTTCTTCTCATGAGGAATGCTGGTCC
CCAGAGCTTGTGGCGCCATCCAGGACTTAAGTCCTACTGTGATCAGTTTGGGCTCGTCT
TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG
CTCTTTTGCAGTGAGCATGAACAGTCCAAAAGCAGTGAATCCACCAGAAGATCAAGCAA
AAAATAAAAGCAAACGTCACTGAAGGCACTGAGCAAATAGCATCCCCGTGAAAAGACACG
AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCAACTGATGGAGAATTTGAATGGTGCAG
ATTAGCAGCAAGGAAGTCTATTCCTTCCCTCCAAACAGAATAATTTCAAGAGATGCTTTAT
TCAAGTGACCGCCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC
AAGATTCCGGGTCTGACAACCAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT
AAGTCTCTCACTCTCTCTCATCATCCGAGTGAGATCTTGGTATAGGTGAACAGAGAACCA
CCCACCTTCCAGAACCAGAACCACCTTCTCCCAAGCCAGCAGTCAGTCACTCACCATCA
GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC
CTACGTCTTTTATAAAACCCAGGTCTTCAGGGCCCCACCCCTTTCTTTTCCATCCTTGCT
CAGAGGCAGCCTTTTGTATACATTCCCTGACCCCAACCCCAATTATATCTCTCATATGATA
TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTGAGATCATTTGCACAAGAACA
AGCGAATACACAACAACAAGCCCACCATCATTACCACCGGCACCTTAATGCTAGTCTTTC
TGCTAGGGATACTGACAGTCTATTTGCTTCCCATGGTCATAGGGAAGTTGCTCAAATGCA
AAGGTTGTAGGGAATGTCTAATTTGTAAATGGCGTCGGGTGCCTTTGGAAGGAATTGTGT
TTTTACAGCCAGTTGCTACTCTTGTATTATCGCTGGTTAACCGGTCTGTCCGGAAGTGAGC
CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCCAGTCCAAAGTCTGCT
TCTCTGTATTTAAATTCTTAGAAGAGTTGCCTGTGGCATTCCAATTGTTATATAAAAAAA
TTATATTAAAGAATTCCAGCACT

SEQ ID NO: 78_AA088547_H

ATGGCGAGTGCGGTTCAGGGGGTTCGAGGCCGTGGCCCCGGCTGGGGCTCCAGCTCCAGTTC
GCGGCGCTGCTGCTCGGGACGCTGAGTCCACAGGTTTCATACTCTCAGGCCAGAGAACCTC
CTGCTGGTGTCCACCTTGATGGAAGTCTCCACGCACTAAGCAAGCAGACAGGGGACCTG
AAGTGGACTCTGAGGGATGATCCCGTCATCGAAGGACCAATGTACGTACAGAAATGGCC
TTTCTCTCTGACCCAGCAGATGGCAGCCTGTACATCTTGGGGACCCAAAAACAACAGGGA
TTAATGAAACTGCCATTACCATCCCTGAGCTGGTTTCATGCCTCTCCCTGCCGCAGCTCT
GATGGGGTCTTCTACACAGGCCGGAAGCAGGATGCCTGGTTTGTGGTGGACCCTGAGTCA
GGGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCCGCCTCTACATTGGC
CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC
ACCTACCGCCGCTACTCAGCGCCCCCATGGATGGCTCACCTGGGAAATACATGAGCCAC
CTGGCGTCTGCGGGATGGGCCTGCTGCTCACTGTGGACCCAGGAAGCGGGACGGTGTG
TGGACACAGGACCTGGGCGTGCCTGTGATGGGCGTCTACACCTGGCACCAGGACGGCCTG
CGCCAGCTGCCGCATCTCAGCTGGCTCGAGACACTCTGCATTTCTCGCCCTCCGCTGG
GGCCACATCCGACTGCCTGCCTCAGGCCCCCGGGACACAGCCACCCTCTTCTCTACCTTG
GACACCAGCTGCTAATGACGCTGTATGTGGGGAAGGATGAAACTGGCTTCTATGTCTCT
AAAGCACTGGTCCACACAGGAGTGGCCCTGGTGCCTCGTGGACTGACCCTGGCCCCCGCA
GATGGCCCCACCACAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT
GGACACCACGAGCTACCCCCAGTCCTGCACACCACCATGCTGAGGGTCCATCCCACCCTG
GGGAGTGGAAGTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG
GAGCTATTGAGCCTGAGCCGAGAGAACTTTGGGACTCCGAGCTGCATCCAGAAGAAAAA
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG
ACCCCCCTGGCACCTGCAGACTTTGCTCACATCTCCCAGGATGCCAGTCCCTGCACTCG
GGGGCCAGCCGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCCAGCCACTC
GACGACCCTGAAGCTGAGCAACTCACCGTAGTGGGGAAGATTTCTTCAATCCCAAGGAC
GTGCTGGGCCCGCGGGCAGGCGGGACTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCCTGGTTCGGCGGGGAAGTTCAACTG
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCGAGCGGGGACCC
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCCTCCTTGCAAGGAGTACGTAGAAAAC
CCGGACCTGGATCGCGGGGGTCTGGAGCCCGAGGTGCTGCTGCAGCAGCTGATGTCTGGC
CTGGCCCCACCTGCACTCTTTACACATAGTGCACCGGGACCTGAAGCCAGGAAATATTCTC
ATCACCGGGCCTGACAGCCAGGGCCTGGGCAGAGTGGTGCTCTCAGACTTCGGCCTCTGC
AAGAAGCTGCCTGCTGGCCGCTGTAGCTTCAGCCTCCACTCCGGCATCCCCGGCACGGAA
GGCTGGATGGCGCCCCGAGCTTCTGCAGCTCCTGCCACCAGACAGTCTTACCAGCGCTGTG
GACATCTTCTCTGCAGGCTGCGTGTCTACTACGTGCTTCTGCTGGCAGCCACCCCTTT
GGAGACAGTCTTTATCGCCAGGCAAACATCCTCACAGGGGCTCCCTGTCTGGCTCACCTG
GAGGAAGAGGTCCACGACAAGGTGGTTGCCCGGGACCTGGTTGGAGCCATGTTGAGCCCA
CTGCCGCAGCCACGCCCCCTTGCCCCCAGGTGCTGGCCCCACCCCTTCTTTTGGAGCAGA
GCCAAGCAACTCCAGTTCTTCCAGGACGTGAGTACTGGCTGGAGAAGGAGTCCGAGCAG
GAGCCCCCTGGTGAGGGCACTGGAGGCGGGAGGCTGCGCAGTGGTCCGGGACAACCTGGCAC
GAGCACATCTCCATGCCGCTGCAGACAGATCTGAGAAAGTTCCGGTCTTATAAGGGGACA
TCAGTGCGAGACCTGCTCCGTGCTGTGAGGAACAAGAAGCACCCTACAGGGAGCTCCCA
GTTGAGGTGCGACAGGCACTCGGCCAAGTCCCTGATGGCTTCGTCCAGTACTTCACAAAC
CGCTTCCCACGGCTGCTCCTCCACACGCACCGAGCCATGAGGAGCTGCGCCTCTGAGAGC
CTCTTCTGCCCTACTACCCGCCAGACTCAGAGGCCAGGAGGCCATGCCCTGGGGCCACA
GGGAGGTGA

SEQ ID NO: 79_HGP_6644466

GGAGGGTTTGAATTGCAACGGCAGCTGCCGGGCGTATGTGTTGGTGCTAGAGGCAGCTGC
AGGGTCTCGCTGGGGGCGCTCGGGACCAATTTTGAAGAGGTACTTGGCCACGACTTATT
TTCACCTCCGACCTTTCCTTCCAGGCGGTGAGACTCTGGACTGAGAGTGGCTTTCACAAT
GGAAGGGATCAGTAATTTCAAGACACCAAGCAAATATCAGAAAAAAGAAATCTGTATT
ATGTTCAACTCCAATAATAATATCCCGGCCTCTCCGTTTATGCAGAAGCTTGGCTTTGG
TACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTG
GGCTGTAAAAAAGATTAATCCTATATGTAATGATCATTATCGAAGTGTGTATCAAAAGAG
ACTAATGGATGAAGCTAAGATTTTGAAGAGCCTTCATCATCCAAACATTGTTGGTTATCG
TGCTTTTACTGAAGCCAATGATGGCAGTCTGTGTCTTGCTATGGAATATGGAGGTGAAAA
GTCTCTAAATGACTTAATAGAAGAACGATATAAAGCCAGCCAAGATCCTTTTCCAGCAGC
CATAATTTTAAAAGTTGCTTTGAATATGGCAAGAGGGTTAAAGTATCTGCACCAAGAAAA
GAACTGCTTCATGGAGACATAAAGTCTTCAAATGTTGTAATTAAAGGCGATTTTGAAC
AATTAAAATCTGTGATGTAGGAGTCTCTTACCCTGGATGAAAATATGACTGTGACTGA
CCCTGAGGCTTGTTACATTGGCACAGAGCCATGGAAACCCAAAGAAGCTGTGGAGGAGAA
TGGTGTATTACTGACAAGGCAGACATATTTGCCCTTGGCCTTACTTTGTGGGAAATGAT
GACTTTATCGATTCCACACATTAATCTTTCAAATGATGATGATGATGAAGATAAACTTT
TGATGAAAGTGATTTTGTATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT
TAATATGGAAGAACTGGATGAATCATAACCAGAAAGTAATTGAACTCTTCTCTGTATGCAC

32/113

FIGURE 2MMM

TAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA
TGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCCTAAATAACTGTTTATTCCAAAATA
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG
TTTCTTGTTAACATATGGATAACTATTTCTAATATGAAATATGCTTATATTGGCTATAAG
CACTTGGAATTGTACTGGGTTTTCTGTAAAGTTTTAGAACTAGCTACATAAGTACTTTG
ATACTGCTCATGCTGACTTAAAACACTAGCAGTAAAACGCTGTAACTGTAACTTAAAT
TGAATGACCATTACTTTTTATTAATGATCTTTCTTAAATATTCTATATTTTAAATGGATCTA
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAAACACTGAACC
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA
GTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGGATCTCCTC
AGATCTTTGGTTTTTGTCTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAAATTTA
TTAATTTGTACCTTAAGCATTTCAGCTGTGTAAAAACAATAAACTCAAATAGGATGA
TAAAGAATAAAGGACACTTTGGGTACCAGAAGGTGTCTCAGCATTATTTTATACTTC

SEQ ID NO: 80_AA449542_M

ATCTCCAAGAGGGTTGTCTCATTCTCCTTGGGCCGTGAAAAAGATAAGTCTTTTATGCGA
TGATCATTATCGAACTGTGTATCAGAAGAGACTAACTGATGAAGCTAAGATTTTAAAAAA
CCTTAATCACCCAAACATTATAGGATATCGTGCTTTTACTGAAGCCAGTGATGGTAGTCT
GTGCCTTGCTATGGAGTATGGAGGTGAAAAGTCTCTGAATGACTTAATAGAAGAGCGGAA
CAAAGACAGTGGAAGTCCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC
AAATGTTGTAATTAAAGGTGATTTTGAAACAATTAAAATCTGTGATGTAGGAGTCTCTCT
GCCATTGGATGAAAATATGACTGTGACTGATCCTGAGGCCTGTTATATTGGTACTGAGCC
ATGGAAACCCAAGGAAGCGTTGGAAGAAAATGGCATCATTACTGACAAGGCAGATGTGTT
TGCTTTTGGCCTTACTCTGTGGGAAATGATGACTTTATGTATTCCACACGTCAATCTTCC
AGATGATGATGTTGATGAAGATGCAACCTTTGATGAGAGTGACTTCGATGATGAAGCATA
TTATGCAGCTCTGGGGACAAGGCCATCCATCAACATGGAAGAGCTGGATGACTCCTACCA
GAAGGCCATTGAACTCTTCTGTGTGTGCACTAATGAGGATCCTAAAGATCGCCCGTCTGC
TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA
TTAACTTGTATGGGAAGTGTAACTAGATATATGTAGTTAATATACTTATGGTAGCTAG
ATTCTAGAAGTAGCTTTAACACTAGTGACCCCTGTCTAAGATGACTTAAGAATCAAGGGA
CCATTGCTTTGTTACAGATCTTTTTAGATATTCTTGCTTCTTTAGTGGGTTACTAAAAAT
TTCCTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTCAGTCCTTCAGCTGGC
CTGTCAGCCCATGCGCCCTGGGACTTGAGAAGAGTTCATAAACGTAGCTCCTAGGGTGTCT
TTGCCTCTCTACACTTAGCTTCTAATTTATTACTTTGTTTCTACTGATTGTGTCTTAAGT
CTTTTAAATAAATGTAAGAATAAACAATAAAAGACAGTTTTTAGTACCAGG

SEQ ID NO: 81_5R57_10_2_M TESK2_M

GCTGCTGGACAGTGACTTGTATTTACCGTGGACTGTGAGAGTGAACTGGCCTATGGCAT
AGCAGTGGGCCTCAGCTACCTTCACTTCAAAGGCATTTTCCATCGGGACCTCACATCAA
GGTGTGAAGGCTTTGCTTTC

SEQ ID NO: 82_AA232253_H

ATGTCGTCTCTCGGTGCCTCCTTTGTGCAAATTAAATTTGATGACTTGCAGTTTTTTGAA
AACTGCGGTGGAGGAAGTTTTTGGGAGTGTATTCGAGCCAAATGGATATCACAGGACAAG
GAGGTGGCTGTAAAGAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTC
AGTCACAGAAACATCATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATT
GTCACAGAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAG
GAGATGGATATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTAT
TTACATATGGAGGCTCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTT

93/113

FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT
ACAACACACATGTCCTTGGTTGGAACCTTCCCATGGATGGCTCCAGAAGTTATCCAGAGT
CTCCCTGTGTCAGAACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTA
ACAAGGGAGGTCCCCCTTTAAAGGTTTGGGAAGGATTACAAGTAGCTTGGCTTGTAGTGGA
AAAAACGAGAGATTAACCATTCCAAGCAGTTGCCCCAGAAGTTTGTCTGAAGTGTACAT
CAGTGTGGGAAGCTGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCATCCTG
GAGTCCATGTCAAATGACACGAGCCTTCCTGACAAGTGTAAGTCAATTCCTACACAACAAG
GCGGAGTGGAGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGAT
CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA
AAGCTGACAGAGCAGTCCAACACCCCGCTGCTGCCTTCCTTTGAGATTGGTGCATGGACG
GAAGACGATGTGTATTGGTGGGTTTACGACGCTCGTCAGAAAAGGTGACTCTTCAGCAGAG
ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG
CTGGAGGAAGAAGACCTGAAAGACATGGGCATTGTCTCCAAGGGGCATATCATTCACTTC
AAGTCAGCCATTGAGAAATTAACCCATGATTACATAAATTTGTTTCACTTCCCACCACTA
ATTAAGGACTCAGGAGGTGAACCTGAAGAAAATGAGGAAAAAATAGTGAACCTGGAAGT
GTTTTTGGTTTTCACTTGAAACCAGGAACTGGCCACAGGATTGTAAGTGGAAAATGTAT
ATGGAGATGGATGGGGATGAAATTGCAATAACCTACATAAAAGATGTGACATTCAACT
AACCTACCTGATGCGGAGATTTTAAAGATGACAAAGCCACCATTTGTAATGGAGAAGTGG
ATTGTAGGAATAGCAAAAAGTCAGACTGTGGAGTGCCTGTACATATGAGAGTGATGTT
AGAACTCCAAAAAGCACTAAACATGTCCATTTGATTCACTGGAGTAGAACAAAACCTCAG
GATGAAGTGAAAGCAGTCCAACCTTGCCATTCAGACATTATTCACCAATTCAGATGGCAAC
CCTGGAAGCAGGTCCGACTCAAGTGCTGATTGCCAGTGGTTAGATACTCTGAGGATGCGG
CAGATTGCATCCAACACTTCTTTACAGCGTTCCCAGAGCAATCCTATTCTGGGGTCACCG
TTCTTCTCACACTTTGATGGCCAGGATTCTTACGCTGCTGCTGTGAGACGGCCCCAGGTG
CCCATTAAGTATCAACAGATTACACCTGTGAACCAGTCCAGAAGCTCGTCTCCTACTCAG
TATGGACTGACCAAAAACCTTCTCTTCTTACATCTCAACTCTAGGGACAGTGGCTTTTCC
AGTGGCAATACTGACACCTCTTCAGAGAGGGGTGATACTCAGACAGAAGCAGGAACAAA
TATGGACGTGGTAGTATATCACTCAATTCTTCTCCTAGAGGAAGATACAGTGGAAGAGT
CAGCATTCCACTCCATCAAGAGGAAGATACCCTGGAAAGTTCTACAGGGTTTCTCAGTCA
GCACTCAATCCTCACCAGTCGCCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC
AACACCATAACCAGGGATGCCTTTGCACCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGGAATACCGGAAAAAGCCCCACAGGCCA
TCTCCCGCCAAAACCAATAAAGAGAGAGCCAGAGGGGACCACCGTGGATGGAGAACTTT
TGA

SEQ ID NO: 83_AI375137_H

ATGGGAAATTATAAATCTAGACCAACCCAACTTGTACTGATGAATGGAAGAAAAAGTC
AGTGAATCATATGTTATCACAATAGAAAGATTAGAAGATGACCTGCAGATCAAGGAAAA
GAACTGACAGAACTAAGGAATATATTTGGCTCTGATGAAGCCTTCAGTAAAGTCAATTTA
AATTACCGCACTGAAAATGGGCTGTCTCTACTTCATTTATGTTGCATTTGTGGAGGCAAG
AAATCACATATTCGAACTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAAT
GGATTTACAGCCTTGCAATTTAGCAGTTTACAAGGATAATGCAGAATTGATCACTTCTCTG
CTTCACAGTGGAGCTGATATACAGCAGGTTGGATACGGTGGCCTCACTGCCCTCCATATT
GCTACAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC
AATATTCAAGATGCAGTTTTTTTCACTCCATTGCATATTGCAGCGTACTATGGACATGAA
CAGGTAAGTGCCTTCTTTTGAATTTGGTGTCTGATGTAAATGTAAGTGGTGAAGTTGGA
GATAGACCCCTCCACCTAGCATCTGCAAAGGATTCTTGAATATTGCAAACCTCTTGATG
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCACTCCAT
TTCTGTTCTCGATTTGGACACCATGATATAGTTAAGTATCTGCTGCAAAGTGATTTGGAA
GTTCAACCTCATGTTGTTAATATCTATGGAGATACCCCTTACACCTGGCATGCTACAAT

94/113

FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG
GAAAACATCTTCAGTGAAACAGCTTTTTCATAGTGCTTGACCTATGGCAAGAGCATTGAC
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG
CACACTGGATTACACTCTGCTTGCTACCACGGTCACATTTCGCCTGGTTTCAGTTCTTACTG
GATAATGGAGCTGATATGAATCTAGTGGCTTGATGCCAGCAGGTCTAGTGGTGAAAAA
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTCACACTC
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA
GGAGATGGCTCCTATGTGTCTGTTCCATCACCCCTTGGGGAAGATTAAAAGCATGACAAAA
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCTTCACATTTCCATCTTCAGCTC
TCAGAAATTGAGTTCCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG
TCAGATGTGGATATGTTTTGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCATCCCTGC
GTAATTTCAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA
TACATATCAGGGGGTTCTCTGTTCTCCCTCCTTCATGAGCAGAAGAGGATTCTTGATTG
CAGTCTAAATTAATTATTGCAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG
ACACAGCCAATTATACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGG
CATGCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC
ATGACAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACGCAGTGCCT
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT
GGCGAAATTCCATTTCGCTCATCTCAAGCCAGCGGCTGCGGCAGCAGACATGGCTTACCAC
CACATCAGACCTCCCATTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA
GGGTGGAACGCATGTCTTGAAGGAAGACCCGAATTTTCTGAAGTTGTCATGAAGTTAGAA
GAGTGTCTCTGCAACATTGAGCTGATGTCTCCTGCATCAAGTAACAGCAGTGGGTCTCTC
TCACCTTCTTCTTCTTCTGATTGCCTGGTGAACCGGGGAGGACCTGGCCGGAGTCATGTG
GCAGCATTAAGAAGTCGTTTGAATTTGGAATATGCTCTAAATGCAAGGTCTTATGCTGCT
TTGTCCCAAAGTGCTGGACAATATTCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG
CATTTTCATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCAGCTGA

SEQ ID NO: 84_H97685_H

ATGATTTCTTGCTGTNATAACCTATGCACTCACAAAGATGAACTCTCTGAGAGGGATGA
GCAAGAGCTTCAGGAAATCCGAAAGTATTTCTCCTTTCCTGTATTCTTTTTCAAAGTGCC
GAAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAAATGGAGAGCGAAAGATCACC
GCTTTATCGCCAGCTAATTGACCTGGGCTATCTGAGCAGCAGTCACTGGAAGTGTGGGGC
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGGAAACAGAGTGAAAAGCTGAGACA
CTTGAGCACATTTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT
GAACCTGGTGCCTGCACTGCCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAAGGAGAATGAGTTGTA
TGAATCATTGATGAATATTGCCAACCGAAAGCAGGAGGAAATGAAGGATATGATTGTTGA
GACACTTAATACCATGAAGGAGGAACCTTCTGGATGATGCTACTAACATGGAGTTTAAAGA
CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG
ACAGATCCAGGAACCTCATCATCTCCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG
CTCAGTGGATTACCTGAGGGAAAGCTTCGTGCGGAACCCCTGGAACGATGTCTGCAGAGCCT
GGAGAAGTCTCAGGATGTCTCAGTTCACATCACAGTAATTATCTCAAACAGATCTTAAA
TGCTGCCTATCATGTTGAAGTCACGTTTCACTCAGGGTCGTGAGTTACAAGGATGCTATG
GGAGCAAATCAAACAGATCATCCAGCGCATCATATGGGTGAGCCCACCTGCCATCACTCT
GGAATGGAAGAGGAAGGTGGCCAGGAAGCCATTGAGAGCCTCAGCGCCTCCAAATTGGC
TAAGAGCATTTGCAGCCAATTCCGGACTCGGCTCAATAGTTCCACAGAGGCTTTTGCAGC
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGTTAGAGAAAACGGAAGATCTATG
GCTGAGGGTTCGGAAGATCATGCTCCCCGCCTGGCCCGCCTTCTCTGGAAGCCGTTT

95/113

FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA
GTATGGTGTGGTATACCTGTGTGACAACTGGGGAGGACACTTCCCTTGTGCCCTCAAATC
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTTCACTATATGAG
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTCAGTCATTGACTACAATA
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA
CACAGGGCTGAAGGCTGGGCTGACCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT
GGAGGGAATCCGCTTCCTGCACAGCCAGGGACTTGTCCATCGTGATATCAAACCTGAAAAA
TGTGCTGCTGGATAAGCAGAACCCTGCCAAGATCACTGACTTAGGATTCTGCAAGCCAGA
GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCCTGAACTTTTCAC
AGGGAAGTACGATAATTCCGTGGATGTCTACGCTTTTGGGAATTCCTTTCTGGTATATCTG
CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG
GAACAATGTGCGGAGGGGGGCTCGCCCAGAACGCTTCTCTGTGTTTGATGAGGAGTGCTG
GCAGTTGATGGAAGCCTGTTGGGATGGCGACCCCTTGAAGAGGCCTCTCTGGGCATTGT
CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTTCACTCTCTAGTTATT
TCCTTCCCCCTCACCATTGCGCCATGGGGAGAATTTGACATTTATTCACTATAGGACACA
CTCCCAAGGGAACCTGGTGCTTGCTGGGAACTTGGAACCTTCCCAGGCAGGGATGACTCC
TGGACAGTGAAGAGTTGAATGACTGAGCATATTCAGCAGCTCACTGAAGCGCCAAGCTAT
CCCTTTAGCAAAAAAGTGTCTCAGATGTGTAAAGCTGAGGAATGTGGTGTCTGGCTTC
ACAAATGAAAAGGAGGCAGATGTT

SEQ ID NO: 85_W20810_M

TTGATGTCAACCTGAAGGCTTCTAAAGCGAGTGATGTCTACAGCTTTGGGATCCTCGTGT
GGGCAGTGCTGGCTGGCAGAGAAGCTGAGTTGGTAGACAAGACTTCACTAATCCGGGAAA
CAGTGTGTGACAGGCAGAGTCGTCCTCCACTGACAGAGCTGCCTCCAGGTAGCCCTGAGA
CTCCCGGCTTGGAAAAACTGAAGGAGTTAATGATTCAATTGCTGGGGTTCCAGTCCGAAA
ACAGGCCATCCTTCCAGGACTGCGAACCACAAAACCAATGAAGTTTACAATCTGGTAAAGG
ACAAGGTAGATGCTGCTGTCTCCGAGGTAAAGCATTATCTGTCTCAGCACAGAAGCAGCG
GCAGAAACTTGTCTGCCAGAGAGCCAAGCCAAAGAGGCACAGAAATGGATTGCCCGAGGG
AAACCATGGTTTCTAAAATGCTGGACCGCCTGCATTTGGAGGAACCTCCGGACCAGTTC
CTGGAAAATGTCCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAGCAA
GGACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCCTTCAGAG
GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCCTCACCCCCAAAGGAATCAGG
GAGATGGAAGACACGGCACTCCTTGGTATCCCTGGACCCCAACGAATCCAATGACAGGGC
CACCGGCTCTCGTCTTCAACAACCTGTTCTGAAGTGCAGATTGGGAACTACAACCTCCTTGG
TAGCACCACCAAGAACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTCGGCA
GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGA
AGTGTGCCATTCAGCGTGGCAATAAAAAGCACGTTTAAAGCAACCTGGACTGGCTAAGAC
AGTCCTTGCCACTTCTGAAGCTCACAACTTCTGTGAGGACAGTTGGACCTACACCCAA
ACTGACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTG

SEQ ID NO: 86_AA744236_H

ATGGGATCAGAGAACAGTGCTTTAAAGAGCTATACACTGAGAGAACCACCATTTACCTTA
CCCTCTGGACTTGCTGTTTTATCCCGCTGTACTGCAAGATGGCAAATTTGCTTCAGTTTTT
GTGTATAAGAGAGAAAATGAAGACAAGGTTAATAAAGCTGCCAAGCATTTGAAGACACTT
CGTCACCCTTGCTTGCTAAGATTTTTATCTTGTAAGTGTGGAAGCGGATGGCATTTCATCTT
GTCAGTACGAGTACAGCCCTGGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCTTCCTTCATGACAGAGGACACCTA
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGACACTGGAAGCTA
GGAGGAATGGAACTGTTTGTAAAGTTTCTCAGGCCACACCAGAGTTTCTGAGGAGTATT

96/113

FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACCT
CTCCCAGAGTGTCTATGGACATGCCCGGGATGCCTTTTTCATTTGGAACATTGGTGGAAAGT
TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC
TTGCACTCAACTTTGCTGAATCCCATTCCAAAATGTGCGCCAGCGCTCTGCACCTTACTA
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAAACA
TTGAAGAGTGAAGAGGAGAAAACGGAATTCTTTAAATTTCTGCTGGACAGAGTCAGCTGC
TTGTCAGAGGAATTGATAGCTTCAAGGTTGGTGCCTCTTCTGCTTAATCAGTTGGTGT
GCAGAGCCAGTGGCTGTTAAGAGTTTTCTTCCTTATCTGCTTGGCCCCAAAAAAGATCAT
GCGCAGGGAGAACTCCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC
GTGCTTCTCCAGTTGTTTGAAGTTCATGAAGAGCATGTGCGGATGGTGTCTGTCTCAC
ATCGAGGCCCTACGTGGAGCACTTCACTCAGGAGCAGCTGAAGAAAGTCATCTTGCCACAG
GTTTTGCTGGGCCTGCGTGATACTAGCGATTCCATTGTGGCAATTACTCTGCATAGCCTA
GCAGTGCTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAACGAACCAAGATC
TTCAAACGCACTGCCCAAGTTTTTACTAAAAATACTGACCTTTTCTCTAGAAGGCGATCCA
TTTTCTCAGCCTATTAAATTTCCCATAAATGGACTCTCAGATGTAAAAAATACTTCGGAG
GACAGTGAAAACCTCCCATCAAGTTCTAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA
CCTGAGGAGCCTGAAAATCAAACCTGTCAACATACAGATTTGGCCTAGAGAACCTTGTGAT
GATGTCAAGTCCCAGTGCCTACCTTGGATGTGGAAGAGTCATCTTGGGATGACTGCGAG
CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT
ACCTCAGGGGAGCAGAAGCCTATTCTGCTTTGCTTTCACTCACTGAAGAGTCTATGCCT
TGGAATCAAGCTTACCCCAAAAGATTAGCCTTGTACAAAGGGGGGATGACGCAGACCAA
ATCGAGCCGCCAAAAGTGTCAACAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT
TTAGGAGAGGAATTCACCATTCAAGTAAAAAAGAAGCCAGTAAAAGATCCTGAGATGGAT
TGGTTTGCTGATATGATCCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA
CTGAGGACAGAAATGGTCCCAAAAAGGATGATGTCTCCCAGTGATGCAGTTTTCTCTCA
AAATTTGCTGCAGCAGAAATTACTGAGGGAGAGGCTGAAGGCTGGGAAGAAGAAGGGGAG
CTGAAC TGGGAAGATAATAACTGGTGA

SEQ ID NO: 87_AI052250_H

AGCGGCCGCGGGGGCGGCGGAGGATATGGAGTAAAGCCAGAGTCAGTGGCCAGGCACGAA
GGCAGAGCAGGAACAGCCAGGAGGCGTTTATTAGGGGGCGGGGGGAAAGAGCCCCAGCA
CCGCCCCCTCCTGGAAGAAGGAAGAGGTAACATACTACCCAATATTGCAGCCATGGAGT
CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGCAG
TAATGGGAATTCCTGTCACTAGAGAATTTGATGTTGGTCGACACATTGCCAGTGGTTGCA
ATGGGCTAGCTTGGAAGATTTTTAATGGCACAAAAAAGTCAACAAAGCAGGAAGTGGCAG
TTTTTGCTTTTGATAAAAAACTGATTGACAAGTATCAAAAATTTGAAAAGGATCAAATCA
TTGATTCTCTAAAACGAGGAGTCCAACAGTTAACTCGGCTTCGACACCCTCGACTTCTTA
CTGTCCAGCATCCTTTAGAAGAATCCAGGGATTGCTTGGCATTTTGTACAGAACCAGTTT
TTGCCAGTTTtagccaatgTTCCTTGGTAACTGGGAAAATCTACCTTCCCCTATATCTCCAG
ACATTAAGGATTATAAACTTTATGATGTAGAAACCAAATATGGTTTGCTTCAGGTTTCTG
AAGGATTGTCATTCTTGATAGCAGTGTGAAAATGGTGCATGGAAATATCACTCCTGAAA
ATATAATTTTGAATAAAAGTGGAGCCTGGAAAATAATGGGTTTTGATTTTTGTGTATCAT
CAACCAATCCTTCTGAACAAGAGCCTAAATTTCTTGTAAAGAATGGGACCCCAAATTTAC
CTTCATTGTGCTTCCAAATCCTGAATATTTGGCTCCTGAATACATACTTTCTGTGAGCT
GTGAAACAGCCAGTGATATGTATTCTTTAGGAACTGTTATGTATGCTGTATTTAATAAAG
GGAAACCTATATTTGAAGTCAACAAGCAAGATATTTACAAGAGTTTCAGTAGGCAGTTGG
ATCAGTTGAGTCGTTTAGGATCTAGTTCACTTACAAATATACCTGAGGAAGTTCGTGAAC
ATGTAAAGCTACTGTTAAATGTAACCTCCGACTGTAAGACCAGATGCAGATCAAATGACAA
AGATTCCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC
AAAGAGATAATCTTCAGAAATCAGAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAAC

97/113

FIGURE 2RRR

TGCCCAAGCGTGTCATTGTGCAGAGAATTTTGCCTTGTTTGACTTCAGAATTTGTAAACC
CTGACATGGTACCTTTTGTGTTTGTCCCAATGTTCTACTTATTGCTGAGGAATGCACCAAAG
AAGAATATGTCAAATTAATTCTTCTCTGAAGTTGGCCCTGTGTTTAAGCAGCAGGAGCCAA
TCCAGATTTTGTAAATTTTCTACAAAAAATGGATTTGCTACTAACCAAAACCCCTCCTG
ATGAGATAAAGAACAGTGTTCTACCCATGGTTTACAGAGCACTAGAAGCTCCTTCCATTC
AGATCCAGGAGCTCTGTCTAAACATCATTCCAACCTTTGCAAATCTTATAGACTACCCAT
CCATGAAAAACGCTTTGATACCAAGAATTAAAAATGCTTGCTACAAACATCTTCCCTTGC
GGTTCGTGTAAATTCATTAAACAACATTGGAGCAGACCTTCTGACTGGCAGTGAGTCCG

SEQ ID NO: 88_AA278842_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCCCCGGCTCGGGCGGCCGGAG
GACCCGGAGCTAAGGCGCCCGAACC CGCGGCGGGCTGGGGACGATGTGGTTCTTTGCCC
GGGACCCGGTCCGGGACTTTCCGTTTCGAGCTCATCCCGAGCCCCCAGAGGGCGGCCCTGC
CCGGGCCCTGGGCCCTGCACCGCGGCCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA
AGCGCTTCAAACTCTACGGCACCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG
AAAAATGCCTCCACGTCTGTGACAGAGGCTGTGACCCCGTTGGGAATATACCTCAAGGCGA
GAGTGGAGGCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGTGA
AAGCCCTCAGCTTCTGGTCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCG
CCGTGTTCTGTGGACCGAGCTGGCGAGTGGAAGCTTGGGGGCTGGACTACATGTATTCCG
CCCAGGGCAACGGTGGGGGACCTCCCCGCAAGGGGATCCCCGAGCTTGAGCAGTATGACC
CCCCGGAGTTGGCTGACAGCAGTGGCAGAGTGGTCAGAGAGAAGTGGTCAGCAGACATGT
GGCGCTTGGGCTGCCTCATTTGGGAAGTCTTCAATGGGCCCCCTACCTCGGGCAGCAGCCC
TACGCAACCCTGGGAAGATCCCCAAAACGCTGGTGGCCCCATTACTGTGAGCTGGTGGGAG
CAAACCCCAAGGTGCGTCCCAACCCAGCCCGCTTCTGTCAGAACTGCCGGGCACCTGGTG
GCTTCATGAGCAACCGCTTTGTAGAAACCAACCTCTTCTGGAGGAGATTTCAGATCAAAG
AGCCAGCCGAGAAGCAAAAATTCTTCCAGGAGCTGAGCAAGAGCCTGGACGCATTCCCTG
AGGATTTCTGTGCGCACAAAGGTGCTGCCCCAGCTGCTGACCGCCTTCGAGTTCGGCAATG
CTGGGGCCGTTGTCTCACGCCCCCTCTTCAAGGTGGGCAAGTTCCTGAGCGCTGAGGAGT
ATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGC
GCATCCGCCCTCTGCAGCAGATGGAGCAGTTTCATCCAGTACCTTGACGAGCCAACAGTCA
ACACCCAGATCTTCCCCACGTCGTACATGGCTTCTTGGACACCAACCCTGCCATCCGGG
AGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATG
TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA
GGGTCTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGCACCGTCCCGGGTTG
CGGGTGTCTTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGA
AGATCCTGCCTGTGCTCTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGG
CCTTCAAGGCCATTCGGAGCTTCTGTCCAAATTGGAGTCTGTGTGCGAGGACCCGACCC
AGCTGGAGGAAGTGGAGAAGGATGTCCATGCAGCCTCCAGCCCTGGCATGGGAGGAGCCG
CAGCTAGCTGGGCAGGCTGGGCCGTGACCGGGGTCTCCTCACTCACCTCCAAGCTGATCC
GTTTCGACCCCAACCACTGCCCCAACAGAAACCAACATTCCCCAAAGACCCACGCCTGAAG
GAGTTCCTGCCCCAGCCCCACCCCTGTTCTTCCACCCCTACAACCTCAGGCCACTGGG
AGACGCAGGAGGAGGACAAGGACACAGCAGAGGACAGCAGCACTGCTGACAGATGGGACG
ACGAAGACTGGGGCAGCCTGGAGCAGGAGGCCGAGTCTGTGCTGGCCAGCAGGACGACT
GGAGCACCGGGGGCCAAGTGAGCCGTGCTAGTCAGGTCAGCAACTCCGACCACAAATCCT
CCAAATCCCCAGAGTCCGACTGGAGCAGCTGGGAAGCTGAGGGCTCCTGGGAACAGGGTT
GGCAGGAGCCAAGCTCCAGGAGCCACCTCCTGACGGTACACGGCTGGCCAGCGAGTATA
ACTGGGGTGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCTGTCTGCACGTC
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCCGAAGAAGCGCGAGGAGCGGCGGCGGGAGA
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCGGA
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGGTGCGGAGAGCCCGCCCCACAGATGT
ATTTATTGTACAAACCATGTGAGCCCGGCCGCCAGCCAGGCCATCTCACGTGTACATA
ATCAGAGCCACAATAAATTCTATTTTCAC

SEQ ID NO: 89_AA599286_H

ATGGCCTTCATGGAGAAGCCGCCAGCCGGCAAGGTGCTGCTGGACGACACGGTGCCGCTG
ACAGCAGCCATCGAGGCGAGCCAGAGCCTGCAGTCCCACACGGAATATATTATTCGAGTG
CAAGGAGGAATTTCTGTGGAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCCTCCCAAAAAATTG
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTAGAT
CCAAACAACATATTCGCAAACTATACTGAGATTGCCTTGCAACAGGTTTCCATGTTCTTC
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACCTTTGAAAGACATAGGTTGGAGAATAAGG
AAGAAATATTTCTTGATGAAGATTAAAAATCAGCCAAAGGAACGGCTAGTGTTAAGCTGG
GCTGACCTTGGCCCCAGACAAGTATTTGTCTAGATAAAGATTTTCAGTGTCTAATCAAACCTT
CTGCCTTCTTGTTTGACCCCTTACATCTATCGGGTTACCTTTGCCACAGCTAATGAATCC
TCAGCGTTGCTAATTAGGATGTTTAAACGAAAAGGGAACATTGAAGGATCTGATCTACAAG
GCAAAACCAAAAGACCCATTTCTAAAGAAGTACTGCAACCCTAAGAAGATTCAGGGCCTG
GAACTCCAGCAAATAAAAAACATATGGACGGCAAATATTAGAGGTACTGAAGTTTCTTCAT
GACAAGGGATTCCCTTATGGGCATCTTCACGCCTCCAATGTGATGCTCGATGGGGACACT
TGCCGGCTGCTGGACCTTGAGAATTCCTTATTGGGCCTGCCTTCCTTCTACCGATCTTAT
TTTTCACAAATTCAGGAAAATCAATACATTGGAAAGTGTGGATGTCCACTGCTTTGGCCAC
TTACTGTATGAAATGACTTATGGACGACCGCCAGACTCGGTGCCTGTGGACTCCTTCCTT
CCTGCCCCGTCCATGGCTGTGGTGGCCGTGTTGGAGTCTACGCTGTCTTGTGAAGCCTGT
AAAAATGGCATGCCTACCATCTCCCGGCTCTTACAGATGCCATTATTCAGCGATGTTTTTA
CTAACCCTTCTGAAAAACCAACAGTTTAAAGATCCCTACAAAGTTAAAAGAGGCATTGAGA
ATTGCCAAAGAATGTATAGAGAAGAGACTAATTGAGGAACAGAAACAGATTCACCAGCAT
CGAAGACTGACAAGAGCTCAGTCCCACCATGGATCTGAGGAGGAAAGAAAAAAGAAAG
ATTTTAGCTCGAAAGAAGTCAAACGATCTGCTCTTGAAAATAGTGAAGAGCATTTCAGCG
AAGTACAGCAACTCCAATAATTCAGCAGGATCTGGGGCCAGCTCACCTCTCACGTCCCCG
TCATCGCCAACCTCCACCCTCTACATCAGGGATATCTGCATTACCTCCACCTCCTCCACCT
CCACCACCACCAGCAGCTCCCTTGCTCTGCGAGCACCAGGCACCTGCCCAGCTCTCG
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCCTTGCTCAGCTCCATCCAGAATTTCCAA
AAAGGAACTTTGAGGAAAGCCAAACCTGTGATCACAGTGCTCCGAAGATCGGCTGAAGCT
TCCTGTTTACACTTGAGGGGAAAAGTTCTTTTTTATTCTACTACCCCTACCCCCAAC
TACCCTCTTCTTGGAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC
AGATGCTCATGTAAGCAGCTTTTCGAGAGAAATAATTCTTTAAGCAGAATAAAGTTAGGC
TGGCATGCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 90_AA425725_H

ATGAGCGCCAGCACGGGCGGTGGTGGGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC
TCACAGGCCCTCTGCGGGCCCGAGTCCTCGGGCTCCGAACTAGCCCTGGCCACACCGGTG
CCTCAGATGCTGCAGGGCCTTCTGGGCTCCGACGACGAGGAACAGGAAGACCCCAAAGAC
TACTGCAAGGGCGGCTACCACCCTGTGAAGATCGGCGACGTGTTCAATGGGCGGTACCAC
GTGGTGCGCAAACCTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCGGGGCATTACACGGAGACAGCT
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCCAAGTGACCCCAAAAGA
GAGACCATTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

93/113

FIGURE 2TTT

TGCATGGTGCTGGAGGTGCTGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACACTAC
CAGGGCCTGCCCCTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCGAGAACATCTTGCTG
TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGGCCACGGAGTGGCAACAGGCA
GGGGCGCCGCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCAGGAGGTCTTGACCGGT
AAGCTGTCCAAAAACAAGAGGAAGAAGATGAGGCGCAAACGGAAACAGCAGAAGCGGCTG
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT
GAGGACTCTGGCTTGAGACTAGACGGGGGACGCGCTCCACATCCTCTTCAGGCTTCTCC
GGCTCCCTCTTCTCTCCTGCCTCCTGCTCCATCCTCTCCGGCTCGTCCAATCAGCGAGAG
ACCGGGGGCCTCCTGTGCGCTAGCACACCATTCGGTGCCTCGAACCTCCTGGTGAACCCC
CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC
GAGCTGGCCACTGGTGACTACCTGTTTCGAGCCGCATTCCTGGAGAAGACTACAGTCGTGAT
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGGACATCCCCCAGCCTTCGCCCTC
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT
CTCAAGCACTGGGGCCTGTACGAGGTACTCATGGAAAAGTACGAGTGGCCCCCTAGAGCAG
GCCACACAGTTCAGCGCCTTTCTGCTGCCCATGATGGAGTACATCCCCGAAAAGCGGGCC
AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

SEQ ID NO: 91_SGK022_H

TCTGGCCCTGTCCCTCCCCACCACCCGCCGCTGTGTCCAGACAGAGAATGTTCTAACGCT
GGGGGCGGCTGCGGATGAAGTCCTTGGGGAGAAAAGGAGCAGGCCAAGGGCGATGGTGA
GTAGAGCTGCCTCTCAGAGGCAGCATGAGCTGAGAGGGTGATAGGAAGGCGGCGCTAGAC
AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG
ACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAACACCAAAGAAAAGTGGCAATTAA
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCTCCCTCGGGAGCTC
CAAATCGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT
GCCGACGGGAAAATCTGCCTGGTGTATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC
GTGCTGAATGGGGGGCCACTGCCTGAAAGCCGGGGCCAAAGGCCCTCTTCCGTCAGATGGTT
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAAC
GCCTTGTGTCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCC
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAG
GTGCTGCAGGGCATTCCCCACGATAGCAAAAAGGTGATGTCTGGAGCATGGGTGTGGTC
CTGTATGTATGCTCTGTGCCAGCCTACCTTTTGACGACACAGACATCCCCAAGATGCTG
TGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT
AGTTGGCATCCATGGCTAGCAAGCACTTGATAAAAGCAATGGCAAGTGCTCTCCAATAAA
GTAGGGGGAGAAAGCAAA

SEQ ID NO: 92_AA060026_M SGK022_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGGGGGGAAAAGA
AGCAGGCCGAGGGCGATGGTGGAGTAGAGCTGCCTCGCAGAGGCAGCATGAGCTGAGAGG
GTGACAAGAAGGAGGCGCTACACAGCATGGAGGACTTTCTACTCTCCAATGGGTATCAGC
TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAAC
ATCAAAGAAAAGTGGCAATTAAAATTATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC
AGAGATTCTGCTCGTGAGCTCCAGATTGTCCGTACCCTGGACCACAAAAACATCATCC
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAAATCTACCTGGTGATGGAAGTGGCTG
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGCCA
AGGCCCTCTTCCGCCAGATGGTTGAGGCTATTGCTATTGCCATGGCTGTGGCGTGGCCC

FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA
GCACAGCCTATGCCGCCCCCTGAGGTGCTACAGGGCATAACCCCATGATAGCAAGAAAGGTG
ATGTCTGGAGCATGGGTGTGGTCCTGTATGTAATGCTCTGTGCAAGTCTACCTTTTGATG
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC
TCCGGCCTTCAATCGAAGAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC
AATGGCAAGTCCTCCCCAATAAAGTAGGGGGAGAAAGCAAAGTCTG

SEQ ID NO: 93_AA399669_H

CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCGCACTTCATTCTCAA
GTTTTGTGGCCAACGATGGATAGGAGGTGGATTGTGATGTATTGGAACATGGGACCTTG
AGGAGTTCCGTAACCAAAAAGGAGAAAGTAACAACAGCCAGTGGAGACAAAAAGAACTGCT
TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGGAGGGCTGAGTCCAGCATCCCAGACTCGT
GTGACTATATAGGCAAGCATTGTTGGGGACCTACTTCACTTTGATACCCTAGCCTTCAGCAG
CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA
AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACCACAGCCTACC
ATTCCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCGCTGAAATACAGGTAA
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC
GAGTATACATCATTTCTGGAAGTGGCTCAGGGTGGTGTATGTCCTTGAATGGATCCAGCGCT
ACGGGGCCTGCTCTGAGCCCCTTGCTGGCAAGTGGTTCTCCCAGCTGACCCTGGGCATTG
CCTACCTGCACAGCAAGAGCATCGTGCACCGGGACTTAAAGTTGGAGAACCTGTTGCTGG
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTGGCTTTTCCCACCTCAGCCAGA
CTTACTGTGGCAGCTTTTGCTTACGCTTGCCAGAGATCTTACGAGGCTTGCCCTACAACC
CTTTCCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTACACTCTAGTGGTGCCTCATC
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT
TCCCAGCTAACCATAACCATCTCCCAGGAGTGCAAGGTCCAAGTCTCATTGCCTGTGTGG
CACAATGGAGAAAACTCAGGCAAGACCTCTCTCTCCCCTGCTCTAGAACCTGATCCTCC
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCTTGGG
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94_AA758539_H

GACCATTGACAGCCTCCGGTAGTGTAATGAGGACAATGCCTGCTGGCCACATGACGG
GGGGATGTAGACGGCAGCGGCCAGTCGCTCCTGGCACCATGGACGATGCCACAGTCCT
AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGCAAGGGTTCTACGCAAAAGTCAA
ATCTGCCTACTCTGAGCGCCTCAAGTTCAATGTGGCTGTCAAGATCATCGACCGCAGGAA
AACACCTACTGACTTTGTGGAGAGATTCTTCCCTCGGGAGATGGACATCCTGGCAACTGT
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC
CCTGCATGAGGACGTGGCAGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGAGAACCTTCTCCTCGACAAGGA
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTGGCAGCATATGCAGCCCCCGAGGTGCT
GCAGAGCATCCCCTACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA
CCTCATCTACCGCATGCTGCAGCCCCGACGTCAGCCAGCGGCTCCACATCGATGAGATCCT
CAGCCACTCGTGGCTGCAGCCCCCAAGCCAAAGCCACGTCTTCTGCCTCCTTCAAGAG
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAACCTGGACACCAAGACAGGCTTGAGGCC
CGACCACCGGCCCGACCACAAGCTTGGAGCCAAAACCCAGCACCGGCTGCTGGTGGTGCC
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG
TGGTGGGGGTGCGGGTTGGGGGGCATGGTGCAGTCGGCCTTCACGTAAACTAAGTAGGCA
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAATTCGTCAATTAAACCACTATTTTGA
TT

SEQ ID NO: 95_AA883975_H

ATGTCGGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCCGCACAATTGGAGAG
GGCAGCTACTCCAAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATC
AAGGTGGTGGACCGGCGGCGAGCGCCCCCGGACTTCGTCAACAAGTTCCTGCCGCGAGAG
CTGTCCATCCTGCGGGGCGTGCGACACCCGCACATCGTGCACGTCTTCGAGTTCATCGAG
GTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC
GTGCAGCGCAACGGGCGCATCCCCGGAGTTCAAGCGCGCGACCTCTTTGCGCAGATCGCC
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCGAAAAC
GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG
GCCCATGGCTACCCAGACCTGAGCACCACTACTGCGGCTCAGCCGCCTACGCGTCACCC
GAGGTGCTCCTGGGCATCCCCTACGACCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC
GTGCTCTACGTATGGTCAACGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
AAGGCCCTGATCGCCGAGCTGCTGCAGTTCAGCCCGTCCGCCAGGCCCTCCGCGGGCCAG
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGACTCCGGCTAG

SEQ ID NO: 96_AA905446_H

CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA
TCATGGAAAGAATTGTGGGGTCAGGGGACAGTGGCGGGAGGAGCTGGCTCACCACCCTGT
GGACAAATCAGGCCTTATAATTTGTGATTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC
TTTTGAATGATATACTAACGACAAAAATAATAGAAGTGAACATTCTTTGCAATGTCCAAG
CAGCTAGACACACTTAAGACCATTAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC
AGAAGTTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCTTTCTGATCTGCCAGCCCAT
CTCTCCTCCCCTTACTTCCTCAGAGTTTATCCAGAGATTCTCCTCGGGAGCTCCAAAT
CGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCTGCCGA
CGGGAAAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT
GAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTCAGATGGTTGAGGC
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT
GTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCCAAGTC
ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT
GCAGGGCATTTCCNNCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCA
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC

FIGURE 2WWW

SEQ ID NO: 97_H29974_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCAGTGGC
CGGGCGCAGCGGGGCCCGGGTGGCGGTCAAGAAGATCCGCTGCGACGCCCCGAGAACGT
GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT
CGTGCAGTTTGAGGAGTGCCTCCTGCAGCGCAATGGGTTAGCCAGCGCATGAGTCACGG
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTTCTGTGAAGGTGG
AGACCTGAATCAGTATGTCCTGTCCCGGAGGCCAGACCCAGCCACCAACAAAAGTTTCAT
GCTACAGCTGACGAGCGCCATTGCCTTCCTGCACAAAAACCATATTGTGCACAGGGACCT
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGA
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTCTGGACTTCTA
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCT
AGAAAACCCAAAGATGGAGTTGCACATCCCCCAAACGCAGGACTTCCATGTCTGAGGG
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCCTGATGCCTT
TGAAGTTGAAACCAGAATGGACCAGGTCACATGTGCTGCTTAAATTCAGGGCTAAGCAT
TTTGGGTGATTTTAACTAGGTCGATTCTCGGGACCCACAGTCTCACCACGTCTCCTCC
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGGTTGGCGATCTCCCGACAGCTGGA
TCCGGCAATGTGAAGCTTTTGTGGGTTTCCCGCTTCTTTTATGTTTTGCTTTATTTN
TNNCCTTTTCTTTTCTTTTNTTTNCCACNTNCCTTTTTTTAAATTTAAACCATTGAG
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTTATAAGGGGTTAGGGAGCTAT
TTTTGGTTTTGTCTTCACTTTCCCTCTGTCTTCTTTTATACTTTTCTCAGTTCTAC
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCCATAGGGAATCTGGGGGTANCT
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG
GAACTCCTGGACTCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA
GAGGTGAAGAACCGCC

SEQ ID NO: 98_AA498104_M H29974_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCGC
AGAGGGACAAAAAGCCCGGAGCGGAAAAGGCGAAGCCAGTCCAGCGGGTACTGTGCGAG
AAGCTGAGGCCGGCGGCCAGGCCATGGATCCGGCTGGGGCCGAGGTCCCGGGCGAGGCC
TTCTGGCCCGCGCGCGCCGGATGGCGGCGCGGGGATGTTCTCTGCACGGCCGCGCTAC
AGCCTCTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCTGTGGCTGGG
CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG
CAGTTTGAGGAGTGCGTCTACAGCGCAACGGGTAGCCAGCGCATGAGTCACGGCAAC
AAGAACTCACAGCTTTACCTGCGCCTGGTGGAGACCTCGCTCAAAGGAGAAAGGATCCTG
GGCTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTACTGTGAAGGTGGAGAC
CTCAATCAGTATGTCCTGTCCCGGAGACCTGACCCAGCCACCAACAAAAGTTTCATGCTA
CAGCTTACAAGCGCCATTGCCTTCCTGCATAAAAACCATCGTGCACAGGGACCTAAAG
CCAGACAACATCCTGATCACAGAGCGGTCTGGCACCCCCATCCTCAAGGTGGCAGACTTT
GGACTGAGCAAGGTCTGTGCAGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGATAAC
AAAAATGTGAATGTGAATAAATACTGGCTGTCTCAGCTTGTGGCTCAGACTTCTACATG
GCTCCCGAAGTCTGGGAGGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC
CTGGGGACCTACATTAAGCAAGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCTAGAA
AACCCAAAGATGGAGTTGCATATCCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGGTC

1-3/113

FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA
CTTGAAACCCGAATGGACCAGGTACATGTGCTGCTTAACTCCAGGGCTGAACGTCTTG
GGTGTTTTTTAACTAGGTTCGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA
TGGCAGAGGGTACAGGTGGTGGTGATCTCCTGACAGCTGGACCTCCCACAATGTGAAGCT
CACGCTTGGGCTGCCCCTCTACCCTTCTCTTTCTCCTTCAGTAGAATAATAATTGTTTT
TCTAAACATTAAACCATCAAGACTTCTGAAGAGCAGAAGGCTACACTCTG

SEQ ID NO: 99_AA215311_H

CGRCCGCGCTACGGAAAGCCGGAGGGGGGCGGGGCCGTGCGCGTAAGGGGGTGTGTCCGC
GCGCACCACGGGGGCGCGCGCCGGCTGCTGACTGGAGGCGGCGGCAGCGAGGCGCGAGC
TGCCCGATAATGGCGGCCTGCAGAGCCCATGAGAGGGAGAAGCGGCAGCGTCTACCCTGA
GAAACCTCGACCTTGAAGATGGTGAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG
GCAGTGAAGAAAATTTCGATGTCACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC
TGGGCACTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC
CTACAAAAGGATGGGATGGTGCAAAGATGTCCCACGGCTCTAATTCTTCCCTTTATTTA
CAGCTTGTAGAACTTCATTAAAAGGAGAAATTGCCTTTGATCCCAGAAGCGCCTATTAT
TTGTGGTGTGTGATGGATTTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG
AAGCCCAATCGTAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC
TTGCATAAAAACCAGATCATCCACCGAGATCTTAAGCCTGATAACATCCTGATTTCTCAA
ACCAGGTTGGATACCAGTGACTTGGAAACCTACCCTCAAAGTGGCTGATTTTGGTCTAAGT
AAAGTTTGTTCAGCCTCTGGGCAGAACCCAGAAGAACCTGTCAGTGTAACAAGTGTTTC
CTTTCACAGCATGTGGAACAGATTTTTTACATGGCTCCTGAAGTTTGGGAAGGACATTAC
ACAGCAAAAGCTGACATCTTTGCTCTGGGGATTATCATCTGGGCAATGCTGGAAAGGATC
ACATTTCATAGACACAGAGACAAAGAAGGAACTCTTGGGGAGTTATGTAAACAAGGAACT
GAGATTGTGCCTGTTGGGGAGGCACCTCTGGAAAATCCCAAATGGAACTTCTCATTCCT
GTGAAGAAAAAATCTATGAATGGGCGAATGAAACAACCTGATTAAGGAAATGCTGGCTGCA
AACCCTCAGGATCGTCCAGATGCTTTTGAAC TAGAACTCAGATTAGTACAAATTGCATTT
AAAGATAGCAGCTGGGAAACGTGACACATATTATTTGCAAATACCATGGATGATATGCTG
CTTCTGTTTAACAGTGATGCAACATTATGTGGCTGAAAAAGAATATAAAAAGCTAGACTC
TACCCTCTAAGGGTTTAGATTTTTTGTGGGATTTTTTTTTTCTCTCATTTTTCTTAAATCC
AAGTTGGCCGTTTTATTAGTATGTTTTCAAATGTGTATTACCAATGTGGGTGTAAATTTTT
AAAAAATGATTATTGATAGAAGTTTGGCAGGAAAATTCTTTAAGAGCTAACAAGAGAAGA
GAGTCCAGTTTTCTGGAAATATGTCTTTAAGTATTTTAGACATTCTCTCGTCAGTATTAGG
AATTTCCATGGGAAAAGAGGTTTGCATGCTGGTAATGCAACCTTTGAAACTTTGTAAAGG
AAACATATATGTATATATTTATGTATATGTAAAGTATGTGAATGTGCGCATTTTGCATTCC
ATATGAAAAAATGCCACGTCTGTTTAAATTATTTGATGTAGGTTTGGGTTTTTGAGATT
TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCTACTCTGCCCCCTCCC
CCTAATGAAATCATATTAAGTNGTTTTCTCTNNTTTTTTTGTAAATATACAGCTTTTTTTT
TAAGGCATCATTTTCGAGGGTCTAAAATTATCTGGTAAACAAATGAAATTAAGTGATCC
AAAGCTGCTGAAGTATGTTTGAACCTCTCCAGTGCCCTATAGCTGCAAGAGTTGAATTAGT
CATGCAGTCATATGGCAGCAGGTGGTGATT

SEQ ID NO: 100_AA018361_H

GCGGGGCTCCGTATCCCCACGTGGGCCCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG
AGGCCAGAGACAGGGGAGGGGCGCCGGGAGCCGGGCGGATCCGCGTCCCCGATGCGCGC
TGCAATTTCCGGCGGGCGCGCTGGGGGACAGCTGGAGCCACCCAGTGCTCGGCCCGCCCC
GCAACCCGCCGGAACCGCCGCCCGCAGCGAGGAAGCGCCCGCGCGGGCGCAGGCGGCCGG
AATGGCGGGGCCCCGCTGGGGTCCCCCGCGCCTGGACGGCTTCATCCTACCGAGCGCCT
GGGCAGCGGCACGTACGCCACGGTGTAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

104/113

FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT
CACGGAGATTGAGATCCTCAAGGGCATTTCGACATCCCCACATTGTGCAGCTGAAAGACTT
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC
TCGCTTCATCCATAACCCGAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA
ATTAGCTAGCGCCCTGCAATTCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC
ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAAACTGGCAGACTTTGGTTT
CGCACAAACACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT
GGCCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCGCGTGGACCTCTGGTCCATGGG
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTCGTTCTCGGA
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGGCGCCCCCTGCTCTC
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCCAGCCGTCGCATCTC
CTTCCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCCAGTGGGGAGAG
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATT
AGCAGCCGCCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGCACTA
TGAAGTGGATGCCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCG
GGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGAGGCAGGGGAC
CTCTGCCCCGAGACCTGCTCAGAGAGATGGCCCCGGGACAAGCCACGCCTCCTAGCTGCCCT
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGGCCCGCGGGGAGCAGGATGCCCT
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCCGGGCCGG
AGGCGGGAGCTGCTTCACACTGAGGTTCAAGACCTCATGGCCCGAGCTGAATACTTGAAG
GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAGAGGGGACTGTGCGAA
TCTGTTTCGTAGCTCTTGACCCCTTCAGTGACCCTAGAAGAATGATTGGACAGATGTGAGC
CATCTGGAGCAGAGGGGCACTAACCCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG
CCCTGGCGAGCAGGCTTCTTGATGGACAGTGCTGAGACCCCCATATCCCAGAGTCCCCA
GCCTCCCTCAGGTTACTCTGCACCCACAGATGGTTTGTATGGCTGTGCTGTATACTGGAG
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTCATGAGACCTTTGTACTCGGTGGT
TACTGGGTCTGTGCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTTGGCTCCGA
GAAGAGGGCAAGGGGCCCCCGCAGGGTACTTCTGTGCTTGCCCTCGCCCTGCCAGCAGGC
AGCTGTGCCCTGGCTGCCCTTCCCGGGACCCCTTATTCCAACCTCAGCTCCTCTTTGCA
CTGGAATGGGGCACTCCAACACCCCTCAGGGACCACCCTCCCCACAGTATGCACTCAGCC
CCACAGAACCCACCAGTCTTTCTGGGAACCTCACACCTGCCCGCCATCTTGGTACTTTAGG
TTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTTAAGAAGCCCAAGCCTTGTTCC
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCCTTGGTCCTCATCTCTCCACCTCCGTT
CCCTCTGGGCCCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGAGCCTGGGACA
GGGAGAGGGAGGCTTGAGACAGTCTGACCCAGTGCCCTCTAGGCCACCCACTTCTAGGC
CTGCCCTGCCGCGTGAGCCCTGGGCAAGCTCTTTCCCCTTTCTGGGCCTGGGTCTCCC
CATCTCTTCAATGGGGCTGATACCTTCACAGCCCACAGCATGGGCACTTATGAGGACAAA
GTGAATTTAACCTGGAAAAGAATGTATTTGAGAGTTTCTTTTAAATAATCAGCGGGTGT
GGTGATTTGTAGCCCTTCTGCCCTTAAATGCTTCCTTGGGCAAGAGCTGTCTGTCTCC
TGCAGGAGGCTGAGTGTGAAGAGTATCATTATTGTTTCTCTATTAAATTATTTTCTCT

SEQ ID NO: 101_AA311714_H

TGGACCTGTCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT
GGACTCTTTTCTTGACTTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATCGTATGTGA
GAAGTCGGCCCAGAGATGGAAAACCTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTTGTAGCCATTCTTTGTACT
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTCACCCGTGAAATAAAACAC
AAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT
GAAAACCTCCCAGAAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGAATTACAT
CATCTTCATAAACTTGGCATTCTCTTTTGTGACATTTCTCCTAGGAAGATACTCTTGGA

FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGATAATGGGGAAAATGTC
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT
GAAATGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTGTTTCAGAATTAAGTGAAG
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCCTAAAGCTTCT
TCAGATTTTATTAATTTGCTTGATGGGTTACTTCAAAGAGATCCTCAGAAAAGATTGACT
TGGACAAGGCTACTGCAGCATTCAATTTTGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA
TCAAGCGTCAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTTCTGGGCCACAAGAT
TCCAAGGAGCTTTTGAGAACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGTGGTCAA
CCACTAGGTCACTCTTTCAGACTAGAAAATCCAAGTGGTTCGGCCTAAGAGTACTCTT
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCCTACTCCCAGAACTAGC
ACTGCAGTGGAAAGTAAGTCCTGGTGAGGATATGACTCACTGTTCAACACAGAAGACTTCT
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGA
GAGCTTATCTACACGGACTCAGATCTTGTTGTACCCCCATTATCGACAATCCAAAGATA
ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCAAGTG
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTTGCAACAAGTGTGCTCG
CAGATCGACTCCACTGAGAAGAGCATGGGGGCTCCCGAGCCAAGCTGAATCTCCTTTGC
TATTTGTGCGTGGTGGCTGGTCACCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTG
TTCCAATTGCTAATCCAGCATTTGCGGATAGCTCCAAACTGGGATATACGGGCCAAGGTT
GCTCACGTGATTGGTTTACTGGCTTCGCACACAAGTGAAGTCCAGGAAAATACACCTGTT
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCAACACTCCACT
CCAGTGCCTAGACAGTGCCTTGTGTATGTATAGATACTGACAAATATTTCAAATAAATA
AAACTGTATCAGCATT

SEQ ID NO: 102_SGK384_H

TCTTTGGCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC
CTGCGGGGCTGGTCAGCGGCTGCGCTACCTGCACCAGCGGTGCATCCTGCACCGC

SEQ ID NO: 103_AA210451_M SGK384_M

GGTCTGCTGCATGGATAATGGACTGGAACACAGAAAGACCATGCAGGGTTCGGCTGTAGA
AGGCCAGTATCTCCAGAGGCCAGAAGACACCATCAGATCTCCTGGGACTGGAGTTATAGA
GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA
AACCCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCGGGGCTGGGGCTGCTGCTCGCCATGG
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCCTGGACGAT
CCACCGCGGACTCTAGGCGCTGTCTCCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT
GCTCACGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT
CCCGGCTCACCAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTC
TCACCGAATATCACCCCTTAGGTTCTTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTCAGCA
TCATTAAGTATCTGCATCACAGCCCCCTGGGCACGAGGGTCATGTGTGACTCTAACGACC
TGCCCAAAACATTGTCCAGTACCTGCTAACAAGTAAGTTCAGCATTGTGGCAAACGACC
TGGACGCTCTGCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT
TCCAAGACGATCTCATGCCTTCCTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG
TCTCCAGTTTCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTTG
ATATCCATAAGGCGTGCAAGAGCCAGATCCCGGCAGAAAGACCCACTGCTCAGAACGTGC

FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTGCGAGACGAAAG
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTACGCC
ACGTAGGCCTCCTCTACGTCTGCCTGCATGTTTGTGAGTGTCTGCTCTCCTGGCAGCCCCG
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG
ATTCTGGATCTGCATAGTTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC
TGCCTTGGTAACTTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGGAC
AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTACAGAAAGCCCTGTTGGAAGCTGGG
GATGTTTTAACTCCGTGGCAGGGCACTTGCCTAGTTGTGTGCAAAGCCTTGGATCTGACC
CATGGCATGTGCACACACAAAATGCTCAAAGAAAATCCCAGACGCCAGAAGTGTGCCCC
TTTCTTGTCAATAAGGTCATTGTTCAGTACCGGAGATGATTTTTTTTTATGAAGCGTTTATG
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTTCTTCTTT
CTTTCTACCCTACTTCTTCCCTTTCCACCCCTAACACTAGATAGGAGAGAGGAGAGAGA
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTCGAGT
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTTCTTCTTGTTCCTTCTCGCC
CACGACCACTTCACAAACACCGACCAACAGCAAACAACCCACCCCGCTTCTCGGGGG
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATCCAATCATCACACACTCAGAG
AAACTGTCTGCTGCTGGCAAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCCACACCTGAGATTAAACAAAAACATT
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG
AGATTGTGGCTGTCTAGAGATTTTTTGAACAGCAAGTTGAAGGAACCTTTCTTACCTGCCT
TGAATGGTGCTTTGAACTTCCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAAA
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG
GAACCAGGAGTTCAGGGTTATCCTGGGCTATATACCGTGACCCTGTCTACCCCCACACCC
CAATAAAAAAACAAAAAGGTC

SEQ ID NO: 104 SGK071_2_H

GAGGTGGTGGCTGTGCAGATGATGGTGGAATGCATGGATGACCATTACGCCAGTCAGGCC
CTGGAGGAGCTGATGCCACTGCTGAAGCTGCGGCACGCCACATCTCTGTGTACCAGGAG
CTGTTTCATCACGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGTGAGGTTT
AATGAGCTCAGCTTCCAGGAGGTCATTGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC
TCTGAGTGGATGCAGAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT
TTGGACATCATCCACAGGAATCTCAAACCCTCCAACATCATCCTCATCAGCAGTGACCAC
TGCAAACCTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT
CGTGCGGAGGAAGACCCCTTTTCGTAAGTCTGGATGGCCCCCTGAAGCCCTCAACTTCTCC
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC
TCCTTCATGGATGGCACAGAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCCAGGC
AGCCTGAAGGCCGCTCCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC
AGGAATCTTCTGCCCTTGATGCTCCAGATCGACCCCTCGGATCGAATAACGATAAAGGAC
GTGGTGCACATCACCTTCTTGAGAGGCTCCTTCAAGTCTCGTGCGTCTCTCTGACCCTG
CACCGGCAGATGGTGCCTGCGTCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC
ATTTTAGGTGATGCTGGGGACACAAAGGGGGAGCGTGCCCTGAAGCTCCTGTCCATGGCC
TTGGCATCCTATTGTTTAGTTCCAGAGGGTTCATTATTTATGCCCTGGCCTTGCTCCAC
ATGCACGACCAAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC
TCCCTGGGGAACTAGGGAAGCTGTTGGGCCCCATCCCAAAGGGTCTGCCGTGGCCCCCG
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCTTCGATGTCCAG
CTGTGTGCCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCACCCGGAA
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCCTGCTGAGTGTCTTTCAGAGCCAC
CCCGAGGAGGAGCCACTTCTTGTCATGGTCTACAGCCTGCTAGCCATCACCAACCCAG

107/113

FIGURE 2BBBB

GAGTCAGAGTCACTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA
AACCACGGAAAGCCCGGAAACCCAAGAACCCTGCCAGCACCCAAAGTATCATTGTGAAC
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG
TCAGAGCTGGCGGCCCTTCAAGGTGGTGGTGCAGGAGGAGGGCGGCAGTGGCCTCAGCCTC
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG
CTGCTGGTCCACCTGGCTTCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTCACCTCCAGCCTGGTGAAGTGACAGCAGC
GCCTTCAGCAAACCAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT
GGGGGACTGGAATAG

SEQ ID NO: 105_AA118352_M SGK071_M

CAGAAGAAGACCCCTGCCAGAAGTCCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT
CCACCAAATCCGACATCTGGTCTCTGGGCTGCATCATTCTAGACATGGCCACTTGCTCCT
TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT
TAGGCAGCTGGCTGTGTGCTTCTTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG
GCTCGCAGAGACTTGGGTTTGATTTTCAGTCAGTCTCTTGGACAGAGCACCCCTCTGAAAG
ATGTCATGCAGAATTTCTCCAGTCGACCAGAGGTCCAGCTCAGAGCCATTAACAAGTTGT
TGACAATGCCAGAGGACCAGCTAGGGCTGCCATGGCCCAACAGAGCTGCTGGAAGAGGTGA
TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC
TGCTGCGTGTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA
GTTTGATCATCTCCTTCCTGATGGATACCTTGCGGAGCCATCCTAACTCTGAAAGGCTTG
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCTGGAGCACTTCCAAGAGGACA
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTCACTGGGTGCTGGCTACTCATC
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTGG
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA
AGGTGTCCGAACCTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCCTGAGGTGGTGGAGAACCTCT
GCATGCTGTTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCCTCTTCAGGC
CCTGACATGCTGCCCTTCTGGTCTGTGGTAAGAGAAAGTATCACTAGGTCCAGTATTAA
TTTCGTACCCCATGGTGAATAATAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106_018653.9_H

GGCCGGGGTCTGGGGCGCGGGGCATGCGCGCGGGCTGGGCAGGGGGCCGGCGGGGCGCAGA
GCGGAGCCGCTCGGAGCCTGAGCCGCCCGGGGCGGGGCGGGGAGCCGCGCGGGGGCCG
GCCGGCCGGGGGAGGGGAGCGATGCGGCGCCGGCGGGCGGCAGTGGCCGCGGGTTTCTG

FIGURE 2CCCC

CGCCTCCTTCCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTTCGGAGCCTCCG
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTCGCGGGGGCCGC
GGGGAGCTGGCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG
GGCCCCGGGCCCCGGGGCGGGCCGGCCGGAGCGGCGGCGCCTGATGGACCTGGCTCCGGGC
GGGCCCCGGCCTGCCGCGCCCCCGGCCCCCTTGGGGCCCGGCCCTGTCCGACGGCGCCCCA
GGCTGGCCCCCGGCTCCCGGCCAGGCTCCCCCGGCCCGGGCCCCGCGCCTGGGCTGCGCC
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC
CGGGTCCGCCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC
GATCTGGGCAGCTGCGTGCGCGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAG
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCAGACACCCTGACCACCATCACG
GAGCTGGGCGCCCCCTGTAGAAATGATCCAGCTGCTGCAAACTTCCTGGGAGGATCGATTC
CGAATCTGCCTGAGCCTGGGCGCCTCCTCCACCACCTGGCCCCACTCCCCACTGGGCTCC
GTCACTCTGCTGGACTTCGCGCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA
CTCGAGTTTCCGGCCAGGAACCTTACCCTGCCCTGCTCAGCCCAGGGCTGGTGCAGGGGC
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTCACATACCTCCTGCCT
CACAGTGCCCCGCCTTCACTGCGTCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG
CTCGCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCA
GACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC
CTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGT
CGGGCCTTTGTGGTCAACCAACCAGACCACCTGGACAGGTCGGCAGCTGGTCTTTTTCAAG
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCTGTG
GAGGGAGTGACTTGCACTGGCAGCACTGCATGTACCTGGGAACCCCTGCAGACAAAGCT
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAT
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT
GACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC
TGTGCCCTCCCTGGGACGGTTCGCTGGGCAGCCCCATCACTGTGTTCAATAGTGTGAGA
ATGTAGCTAAAGCCCCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGCTGCG
TGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG
GGGACACTCCCAGGCCAGCCCAGGGGTGAGGGGAGAGGTGCACACCTCAGCATGAGCCA
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG
GGCCTTCTGCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACAGGCTTTCC
CCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTAT
TTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACCTCTCCC
T

SEQ ID NO: 107_AA396601_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGTCTGGCGCGCAGTACGTGGGCTCAG
GCTACACTAAGGCTGTGTACCGGGTCCGCCTGCCCGGCGGCGCCGCGGTGGCGCTTAAAG
CAGTGGACTTCAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCGGGGCGCGAAGGG
GCTGCTATCGCCTGGCGGCCCAAGCTGCTCAAAGAGATGGTGCTGCTGGAGCGGCTGC
GGCACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCAG
ACACGCTGACCACCATCACAGAGCTGGGTGCCCTGTGGAGATGATCCAGCTGTTGCAGA
CTTCTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCCTCCTCCACCACCTGG
CCCACTCCCCGCTGGGCTCGGTACCCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACTTCAGCCTGCCCTGCTCGG
CCCAGGGCTGGTGCAGGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT
TCTTCACATACCTCCTGCCACACAGTGCCCCGCCTTCCCTCCGACCTCTCCTGGATAGCA
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCAGCTGGAGA
CAGCGCTACACTTGTTCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG
AGTACCAGCGCATCCCGGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG
AGAGCCATGCTCAGTGTCGTGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGA
AGCTGGTCTTTTTTAAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT
ATGTGAAGGCCCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCTGTG
CAGGCGTGACTTGTCATCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA
CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAAATCTGAGTTTGCCAGC
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG
CTCAGGCTGGTCTTAACTGGGACAGTCCCGTGGGCAGCCCATTACTGCATTTCATGCTTTG
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG
CCTCATTTGCTTTCAGTGAAAGCCAGGGAGCAGCCGCAGCCAGGCTCCTCCCCTCCTGG
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC
CAGAAGCTTTTATACTTCTCGTTTCATTAAATTGTTTATTTTTGTAAAAAAAATTAAT
CAATTAATAAAATGATGTTTTGTGAC

SEQ ID NO: 108_VRK3_H

ATGATCTCCTTCTGTCCAGACTGTGGCAAAAGTATCCAAGCGGCATTCAAATTCTGCCCC
TACTGTGGAAATTCTTTGCCTGTAGAGGAGCATGTAGGGTCCCAGACCTTTGTCAATCCA
CATGTGTATCCTTCCAAGGCTCAAAGAGAGGGCTGAACTCCAGTTTTGAAACCTCTCCT
AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCTCTGAGAGATCCAAAGGCTCCGGGAGC
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCCCACAGGGACAGTGCTGACAGAC
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC
TATGAAGCTGCACCCACCTCCACCCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG
GCCGCCAAGCCTCTGCAAGTCAACAAGTGGAAGAAGCTGTACTCGACCCCACTGCTGGCC
ATCCCTACCTGCATGGGTTTCGGTGTTCACCAGGACAAATACAGGTTCTTGGTGTACCC
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTCAGCCCAAAGCATGTGCTGTCAGAG
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCTTCCATGAGAA
GAGTATGTTTCATGGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAACACGTG
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTTCATTAGCATGGAC
CTGCACAAGGGATGCGGGCCCTCCCGCCGCAGCGACCTCCAGAGCCTGGGCTACTGCATG
CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATTGCCTTCCCAACACTGAGGACATC
ATGAAGCAAAAACAGAAGTTTGTGTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTCAC
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGTGAGCCCTCACGTAT
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG
CGTGTGTCTCCATATGACCCCATTTGGCCTCCCGATGGTGCCCTAG

FIGURE 2EEEE

SEQ ID NO: 109_S71575_M VRK3_M

CCATCCCCACCTGTATCGGCTTTGGCATTACACAGGACAAGTACAGGTTCCCTAGTATTCC
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG
AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA
ATGAGTATGTTTCACGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA
GCCAGGTGACCCTGGTGGGCTATGGCTTCACCTACCGATACTGCCCAGGTGGCAAACACG
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG
ACCTGCACAAGGGATGCGGACCCTCCCGCCGACGCGATCTCCAGACCTTGGGCTACTGTA
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGATGGCCCTCAATT
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA
TGCGGGTGTCACCCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG
CTTCCGACTTGCAGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAAC
CATAGCTCCTAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTCATGTAATGTGAACTCCTCCCTGTCTC
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGAGCAGCCAC
TCCACTCCCTATGGCATTCTGTGATGGCATAATAAACTGTTTTTAATC

SEQ ID NO: 110_AA45427_H

ATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAAGTGTGTCATTGACAATAAGCGCTAC
CTCTTCATCCAGAACTGGGGGAGGGTGGGTTCAGCTATGTGGACCTAGTGGAAGGGTTA
CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTCACGAGCAGCAGGACCGGGAG
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG
ACCGAGGATCAAATCCTTTGGCTGCTGCTGGGGATCTGCAGAGGCCTTGAGGCCATTCA
GCCAAGGGTTATGCCACAGAGACTTGAAGCCACCAATATATTGCTTGAGATGAGGGG
CAGCCAGTTTTAATGGACTTGGGTTCATGAATCAAGCATGCATCCATGTGGAGGGCTCC
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCAGCGGTGCACCATCTCCTACCGAGCC
CCAGAGCTCTTCTCTGTGCAGAGTCACTGTGTCATCGATGAGCGGACTGATGTCTGGTCC
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTCCAA
AAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGCATCCACAAAGCCCCAGG
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT
CCTCACATTCTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCCAGCTCCTGGCCAA
CATACTACCCAAATCTGA

SEQ ID NO: 111_H05721_H

CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGGACGCCGGTGGTGGCGGCAGC
GACGGCTGCGGGGGCACC GGCGCGGCCACCATGGCGGTGCGACAGGCGCTGGGCCG
CGGCCTGCAGCTGGGTTCGAGCGCTGCTGCTGCGCTTCACGGGCAAGCCCGCGGGCCTA
CGGCTTGGGGCGGCGGGCCCGCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTCGGGCTCGGGCTCCCTAACCGTCTCCGCTT
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGCAGTTCGTGGTGGCGGC
CTGGGGCTGCGCGGGCCCTTGCGGCGGGCAGTCTTTCTGGCCTTCGGGCTAGGGCTGGG
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGAGATCCA
GGCAATTTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA
GGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGTGCTG
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACCGG
GTTGCTTCCAGGGAGAGGGCCAGGTACCAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCC

FIGURE 2FFFF

GGGGGCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCTC
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTT
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC
CCCTCAGCCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCGCTGCTGCC
AGGGGCCCCTGGTTCGACTACCCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG
CCATGGCCGGACGCTGTTCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT
TGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCT
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGCGG
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCTGGCCCCAGGGCAGTGAT
TGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCCGGGCT
TGTCATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGCAGCTACCAAGAGGC
TCAGCTACCTGCAGTCCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG
CTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTTG
TGTGGAACAACAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTGAAACGCTCTGCCA
GGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT
GAATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGG
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAAAAGGCCCTCGGGCTTGG
CAAATGGAAGAACTTGAGTGAGAGTTTCACTCTGCAGTCCCTCTGCTCACAGACATCTGAAA
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTCAGTGGCAGAGTTTGGCTGTGACCTTT
GCCCCTAACACGAGGAACCTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG
GATGAAGGCAGACATCAACATGGGTTCAGCACGTTTCACTTACGGGAGTGGGAAATTACATG
AGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTGGGGATTTAAACTTGAG
GGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAATGCAAATTTACA
ACTGCAGATGACGTATGTGCCTTGAAGTGAATATTTGGCTTTAAGAATGATTCTTCTTAT
ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAAGAGATTTTCATGTC
TAACTAACTAACTTTATACATGATTTTTTAGGAAGCTATTGCCTAAATCAGCGTCAACATG
CAGTAAAGGTTGTCTTCAACTGACAAAA

SEQ ID NO: 112_AI086865_H

AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG
CACCTGTGCCTGCGAAAGGCTGACCAGAAGCTGGTGATCATCAAGCAGATTCCAGTGGA
CAGATGACCAAGGAAGAGCGGCAGGCAGCCAGAAATGAGTGCCAGGTCTCAAGCTGCTC
AACCACCCCAATGTCATTGAGTACTACGAGAAGTTCCTGGAAGACAAAGCCCTTATGATC
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTTCACTCCAAAAGCGCTGTAATTCC
CTGCTGGAGGAGGAGACCATCCTGCAGTTCTTCGTGCAGATCCTGCTTGCAGTGCATCAT
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA
CACCGCATGGTTCGTCAAGATCGGTGATTTTCGGCATCTCCAAGATCCTTAGCAGCAAGAGC
ACCCCATGCTATATCTCCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAAGAGTGAC
ATCTGGGCCCCTGGGCTGTGTCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTCGAGGCT
GCGAAGTTGCCAGCACTGGTGCTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCTGAGTCTACTCAGCCTGGAGCCTGCCAG
CGGCCACCACTCAGCCACATCATGGCACAGCCCTCTGCATCCGTGCCCTCCTCAACCTC
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACAGTGT
CCGCTGCAGAGAGGCATCATCATGACATTCGGCAGCGGCAGCAATGGGTGCCTAGGCCAT

FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCACCATTTGTGGAGGCTTTGTTGGGCTATGAAATG
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACACTACTAGGCTCTGCACCCCTGGACCAG
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC
AAGTGCTGCTGGAGACACAAGCAGTGCCTGGGCACATCATCTACCCTTTTCGCCTCTGAC
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCACTGCAACTGTAATTCTAGGCTG
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGCGGGCCCAACCTGCTCCCATGTC
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT
GGCTGGTGCAAAAGCTACAGACCTGTCTCTGTGGCAGTGATCCACCATCCACTCTACCAT
GAGTGTGGGGCAGATGATCTAAATGXAAAGAAGAGGAAGAGGAGGAGGAGGAGGAAAAGCAAG
CCCCCATCCCGACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACCAGCATG
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAAGCCAAGAAAGGCCAGTTG
ACTAAGAAGAAAAGCCCGGTTAAATTGGAGCCTTCCCCGCCAGACGTGAGCCGATCATT
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCCAGAAAGCCGGGAAGAGCTGGAG
AGCGAGGACAGTTACAATGGCCGGGGGCGAGGAGAACTGTCCAGCGAGGATATTGTGGAA
TCATCATCGCCAGGAAGAGAGAGAAACACAGTCCAGGCCAAAAAGACAGGGGCAAAGCCC
TCACAAGCCAGGAAGGTAAACAAGAGAAAATCTCCCCAGGATCAAACCCCAACCTCAGT
TGAGGCCAGGGTGGTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG
CAGGGGTTTCTCAAAGGCAATCCAGCTTTTCAAAAGGAAGCCCATGGGAAGGCAGGTGGG
AGGGAAAGGAAGGGGCACAGCCCTATTTCTTCTTACCTGCTAGGACAAGGTGGAAGAGTG
TATCTGGGGTGGGAAGGAGGGCTTCCCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT
CCACTTCTGGGACAGGCAGTACTGTCTGCAGCGATACCCCCAATAAACGGAACCTTTTAA
CCC

SEQ ID NO: 113_AA836348_H

ATGTCGGTGCTGGGCGAGTACGAGCGACACTGCGATTCCATCAACTCGGACTTTGGGAGC
GAGTCCGGGGGTTGCGGGGACTCGAGTCCGGGGCCTAGCGCCAGTCAGGGGCGCGAGCC
GGCGGCGGCGCGGCGGAGCAGGAGGAAGTGCCTACATCCCCATCCGCGTCTGGGCCGC
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGACCGAGGATGACTCACTGGTTGTGTGG
AAGGAAGTCGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA
GTTATTCTGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC
CTTCGTCAGAAGGACAAGTTGTTTGAGGAAGAGATGGTGGTGTGGTACCTATTTTCAATT
GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA
AATATTTTTCTGACCAAGGCAAACCTGATAAACTTGGAGATTATGGCCTAGCAAAGAAA
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCCATATTACATGTCTCCA
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT
GTGAAGATCGTGCAAGGAATTCGGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA
TTGATCCAAATGGTTCATTTCGTGCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT
GAACCTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA
CCCATTGCTGTAGTAACATCACGAACCAAGTGAAGTCTATGTTTGGGGTGGTGGAAAATCC
ACCCCCCAGAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG
AATACCCACTTTGCTGTGGTTCACAGTGGAGAAGGAAGTGTACACTTGGGTGAACATGCAA
GGAGGCACTAAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA
AAGCATGTGGAAGGTTGCAAGGCAAAGCTATCCGTCAGGTGTGATGTGGTGTGATTTT

FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACTTCTTC
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA
AACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTTCAGAA
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGAATTATCAACCATGAA
GCATACCATGAAGTTCCCTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT
AAGATCCGTACCATTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG
CTGCTGACCTTTGGCTGCAACAAGTGTGGGCAGCTGGGCGTTGGGAACCTACAAGAAGCGT
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT
TCCAATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAACTCCTGACCCA
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAAATCAGTCCC
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCTGGCTGGCTTCGAAAG
GAGCTGGAAAATGCAGAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG
TTTTTCAGAACTCTGAGAAAGATACCCCTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAAGTGAAGCTTTTGGCC
TTTGAATCACAACTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

SEQ ID NO: 114_R86668_H, MKK6_H

ATGAACTTGCTGCTCTCCTACCGCGATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG
GAGACGCTGCAGGCCTTGCCACCTGTGATGTGGCCGAGCAGCATAATGTCTGCTTCCAC
TACACTTTTGCCCTCAACCGGAGGAACAGGCCTGGGGACCGGGCGAAGGCCCTGTCTGTG
CTGCTGCCGCTGGTACAGCTTGAGGGCTCTGTGGCGCCCGATCTGTACTGCATGTGTGGC
CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCCAGCCTTCACTCAGGCATCAAT
GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAAGAGCTCCGGCTA
ATAGGCATGAAGCTGGGCTGCCTGCTGGCCCGCAAAGGCTGCGTGGAGAAGATGCAGTAT
TACTGGGATGTGGGTTTCTACCTGGGAGCCAGATCCTCGCCAATGACCCACCCAGGTG
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCCATATGGTACCTGGTGTCCGTG
ATGGAGACCTTCTGCTCTACCAGCACTTCAGGCCCAGCCAGAGCCCCCTGGAGGGCCA
CCACGCCGTGCCCACTTCTGGCTCCACTTCTTGCTACAGTCTTGCCAACCATTCAGACA
GCCTGTGCCCAGGGCGACCAAGTGCTTGGTGCTGGTCTTGAGATGAACAAGGTGCTGCTG
CCTGCAAAGCTCGAGGTTCCGGGTACTGACCCAGTAAGCACAGTGACCCTGAGCCTGCTG
GAGCCTGAGACCCAGGACATTCCCTCCAGCTGGACCTTCCAGTCGCCTCCATATGCGGA
GTCAGCGCCTCAAAGCGCGACGAGCGCTGCTGCTTCTCTATGCACTCCCCCGGCTCAG
GACGTCCAGCTGTGCTTCCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG
GCCTGGGTGACGAACCCGATTCCACGGCGCCCGCGGAGGAGGCGGAGGGGCGGGGGAG
ATGTTGGAGTTTGATTATGAGTACACGGAGACGGGCGAGCGGCTGGTGCTGGGCAAGGGC
ACGTATGGGGTGGTGTACGCGGGCCGCGATCGCCACACGAGGGTGCGCATCGCCATCAAG
GAGATCCCGGAGCGGGACAGCAGGTTCTCTCAGCCCTGCATGAAGAGATCGCTCTTAC
AGACGCCTGCGCCACAAGAACATAGTGCGCTATCTGGGCTCAGCTAGCCAGGGCGGGCTAC
CTTAAGATCTTCATGGAGGAAGTGCTTGGAGGCAGCCTGTCTCCTTGCTGCGGTGCGTG
TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG
GGACTTGGCTACTTGCACGACAACCACATCGTGCACAGGGACATAAAAGGGGACAATGTG
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG
GCAGGCATCACACCTTGCACTGAGACCTTCACAGGAAGTCTGCAGTATATGGCCCCAGAA

FIGURE 2III

ATCATTGACCAGGGCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC
ACTGTCATTGAGATGGCCACAGGTCGCCCCCCTTCCACGAGCTCGGGAGCCACAGGCT
GCCATGTTTTAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCAGCTCTCTGTGGCC
GAGGCCCAAGCCTTTCTCCTCCGAACTTTTGAGCCAGACCCCGCCTCCGAGCCAGCGCC
CAGACACTGCTGGGGGACCCCTTCTGTCAGCCTGGGAAAAGGAGCCGAGCCCCAGCTCC
CCACGACATGCTCCACGGCCCTCAGATGCCCCCTTCTGCCAGTCCCCTCCTTCAGCCAAC
TCAACCACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCTCTCAGCACCCACCCAGC
CCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTGCGGGCTGAGCCTGCTGCACCAGGAG
AGCAAGCGTCGGGCCATGCTGGCCGAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCGTCTGGGCAGAAACCATGTGGAA
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGGCAGCTCGCCAG
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGCCCAGGGCCTTGGGCCTGCGCTTCTGCAC
AGACCGCTGTTTGCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT
CCACACTGGATGTTCTGTTCTGGAATCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT
GTGCTAGGACCGGAGGTGGAGAAGGAGGCGGTCTCACCGAGGTGAGAGGAGCTGAGTAAT
GAAGGGGACTCCCAGCAGAGCCCAGGCCAGCAGAGCCCGCTTCCGGTGGAGCCCGAGCAG
GGCCCCGCTCCTCTGATGGTGCAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGCAGCGGGCTCTACAGCGG
CTGAATGAGGAAGCCCGGACCTATGTCCTGGCCCCAGAGCCTCCAACCTGCTCTTTCAACG
GACCAGGGCCTGGTGCAGTGGCTACAGGAAGTGAATGTGGATTGAGGCACCATCCAAATG
CTGTTGAACCATAGCTTCAACCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

SEQ ID NO: 115_PAK6_H

ATGTTTGGGAAGAAAAAGAAAAAGATTGAAATATCTGGCCCCGTCCAACCTTTGAACACAGG
GTTTACTACTGGGTTTGATCCACAAGAGCAGAAGTTTACCGGCCTTCCCCAGCAGTGGCAC
AGCCTGTAGCAGATACGGCCAACAGGCCAAAGCCTATGGTGGACCCTTCATGCATCACA
CCCATCCAGCTGGCTCCTATGAAGACAATCGTTAGAGGAAACAAACCCTGCAAGGAAACC
TCCATCAACGGCCTGCTAGAGGATTTTGACAACATCTCGGTGACTCGCTCCAACCTCCCTA
AGGAAAGAAAGCCCACCCACCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG
GAAGAAAATGGCTTCATCACCTTCTCCCAGTATTCCAGCGAATCCGATACTACTGCTGAC
TACACGACCGAAAAGTACAGGGAGAAGAGTCTCTATGGAGATGATCTGGATCCGTATTAT
AGAGGCAGCCACGCAGCCAAGCAAAATGGGCACGTAATGAAAATGAAGCACGGGGAGGCC
TACTATTCTGAGGTGAAGCCTTTGAAATCCGATTTTGCCAGATTTTCTGCCGATTATCAC
TCACATTTGGACTCACTGAGCAAACCAAGTGAATACAGTGACCTCAAGTGGGAGTATCAG
AGAGCCTCGAGTAGCTCCCCTCTGGATTATTCAATTCCAATTCACACCTTCTAGAAGTGA
GGGACCAGCGGGTGCTCCAAGGAGAGCCTGGCGTACAGTGAAAGTGAATGGGGACCCAGC
CTGGATGACTATGACAGGAGGCCAAAGTCTTCGTACCTGAATCAGACAAGCCCTCAGCCC
ACCATGCGGCAGAGGTCCAGGTCCAGGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA
GCAAGTGCATTTAAAACCCATCCCCAAGGACACTCCTACAACTCCTACACCTACCCTCGC
TTGTCCGAGCCCAATGTGCATTCCAAAGGTGGATTACGATCGAGCACAGATGGTCCTC
AGCCCTCCACTGTCAGGGTCTGACACCTACCCAGGGGCCCTGCCAACTACCTCAAAGT
CAAAGCAAATCGGGCTATTCTCAAGCAGTACCAGTACCCGTCTGGGTACCACAAAGCC
ACCTTGTAACCATCACCCCTCCCTGCAGAGCAGTTTCGAGTACATCTCCACGGCTTCTAC
CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCAGCTGGGGCTCCTCCTCC
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGGCCCTGCAGCTGGTGGTC
AGCCCAGGAGACCCAGGGAATACTTGGCCAACTTTATCAAAATCGGGGAAGGCTCAACC
GGCATCGTATGCATCGCCACCGAGAAACACACAGGGAAACAAGTTGCAGTGAAGAAAATG

FIGURE 2JJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT
TACCACCATGACAATGTGGTTGACATGTACAGCAGCTACCTTGTCGGCGATGAGCTCTGG
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAT
AACCAAGGAGTGATTACAGGGACATAAAAAGTGACTCCATCCTCCTGACAAGCGATGGC
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG
AAATCATTGGTTGGCACTCCCTACTGGATGGCCCCTGAGGTGATTTCTAGGCTACCTTAT
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG
CCCCCTACTTCAATGAGCCTCCCCTCCAGGCGATGCGGAGGATCCGGGACAGTTTACCT
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCTTAGACTTGATG
TTGGTGAGGGAGCCCTCTCAGAGAGCAACAGCCCAGGAACTCCTCGGACATCCATTCTTA
AAACTAGCAGGTCCACCGTCTTGCATCGTCCCCCTCATGAGACAATACAGGCATCACTGA

SEQ ID NO: 116_SURTK106_H

ATGAATGATAGGAATGAGATTCAAATGGAAGCCAAACTCCAAAGTCTTACCATTATAGCA
CAGGAAATTCTATGCAGATTCTTTATTACCCTTAGGAGACATGCACGTTTCTTGCTCACT
AAACTAGGAAGGCAAGGAATGGCAAGGTCAGGAATTACTCACAGCTGTGCTGTGTGCATT
CTCTGTGGGCCCTAGCAGGGAAGGGGACAGCCCTGTGGCAATGGGCATGACACGGATGCTC
CTGGAATGCAGTCTCAGTGACAAGTTGTGTGTCATCCAGGAGAAGCAGTATGAAGTGATT
ATCGTCCCAACTTTTGTGGTTACTATCTTCCCTCATCCTTCTTGGGGTCATCCTGTGGCTT
TTTATCAGAGAACAAAGAACTCAACAGCAGCGTTCTGGACCTCAAGGCATTGCCCCTGTT
CCTCCACCTAGGGACCTAAGCTGGGAAGCAGGACATGGAGGAAATGTGGCTTTGCCACTT
AAGGAGACATCCGTGGAAACTTTCTGGGAGCTACCACACCTGCCCTGGCTAAGCTGCAG
GTGCCGCGGGAGCAACTCTCTGAAGTTCTGGAGCAGATTTGCAGTGGTAGCTGTGGGCCC
ATCTTTTCGAGCCAATATGAACACTGGGGACCCTTCTAAGCCCAAGAGTGTTATTCTCAAG
GCTTTAAAAGAACCAGCTGGGCTCCATGAGGTACAAGATTTCTTAGGGCGAATCCAATTC
CATCAATACCTGGGGAAACACAAAAACCTGGTGCAGCTGGAAGGCTGCTGCACTGAAAAG
CTGCCACTCTATATGGTGTGGAGGATGTGGCCCAGGGGGACCTGCTCGGCTTTCTCTGG
ACCTGTGCGGCGGGATGTGATGACTATGGATGGTCTTCTCTATGATCTCACAGAAAAACAA
GTATATCACATCGGAAAGCAAGTCCTTTTGGCGCTGGAATTCCTGCAGGAGAAGCATTTG
TTCCATGGGGATGTGGCAGCCAGGAATATTCTGATGCAAAGTGATCTCACTGCTAAGCTC
TGTGGATTAGGCCTGGCTTATGAAGTTTACACCCGAGGGGCCATCTCCTCTACTCAAACC
ATACCTCTCAAGTGGCTTGCCCCAGAACGGCTTCTCCTGAGACCTGCTAGCATCAGAGCA
GATGTCTGGTCTTTTGGGATCCTGCTCTATGAGATGGTGACTCTAGGAGCACCACCGTAT
CCTGAAGTCCCTCCTACCAGCATCCTAGAGCATCTCAAAGAAGGAAAATCATGAAGAGA
CCCAGTAGCTGCACACATAACCATGTACAGTATCATGAAGTCCTGCTGGCGCTGGCGTGAG
GCTGACCGCCCCCTACCTAGAGAGCTGCGCTTGCGCCTAGAAGCTGCCATTAAAACTGCA
GATGACGAGGCTGTGTTACAAGTACCAGAGTTGGTGGTACCTGAACTGTATGCAGCTGTG
GCCGGCATCAGAGTGGAGAGCCTCTTCTACAACTATAGCATGCTTTGAAGAGTCTCGGGC
AAGAAACATTCATGCATGAGTATATGTTCTTGGAATCAATTCTCTAAGAACAGAGAATG
GTCTTTCCCAGGGACACAAAGGGAGAAATGGGACATGGATTCTTGATCTTCTTTACACA
TTTCTCGGGAAATCTGAAATGATGCTGGATGGGACTCTACACATCCTGAGCTAAGACATA
CTGTCACTCTCACTTCTGCTGTCCAGTCCTAGAAATCCTGGGTAGAAGTGGTGGACCTG
TGCAAAGGAGGTTTTAGAACTCTGCAGTATTTGTTGGGGCATGGCACAAATAAGCTCATC
CCTCCCGTCCGAGGCTAGTTTCTCTGGAACCACATTTTTATCTAGATGAAAATTTGGAA
TGAAATGAAGGAATAGAAATCCAATAAAAGAGTTGAAGGGAAAGAAAATTTAAGGTTCTT
CTTGCTCAGGATTACAGATATGGACCAACACCTCCTTCAAGAAAAGGTGGTAGGACACAA
AGTTCTTCAGTCCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC
TGAGTTTCACCTTAGGTATAGATAAAAGAAAGATGGTCCCCTTTTATCTGATTCTGAGAC
AGGTAAATTCTGTTTGTACTACGTTTAATTAGAAGGTGGAGGAGTCATTTTCATGATTAA

FIGURE 2KKKK

GAACATTCAACATGTATTGTTTATTAAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAAAGAATTCTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGCACAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA
GTCTTTAACAAGGGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATT
TTCAATCATCTGTTGATATACTGTGAAACTTATTTTATTAAATTAATATTTATTAAATGG

SEQ ID NO: 117_AA098024_M

CTGCAGGAGAAGCACCTGTTTCATGGGGATGTGGCTGCCAGGAACATCCTGATCCAAAGT
GACCTGACTCCCAAACCTTTGTTCATCTGGGCCTGGCTTATGAAGTTCATGCCCATGGGGCC
ATCTCCTCTGCTCGATCCAGCACCATCCCTCTCAAGTGGCTTGCTCCAGAAAGGCTTCTC
CTGAGACCTGCAAGCATCAGGGGAGATATTTGGTCCCTTGGGATCCTGCTTTATGAGATG
GTGACTCTAGGAGCACCACCATAACCCTGAAGTCCCTCCCACCAGCATCCTACAATATCTT
CAGAGAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG
AAGTGCTGTTGGCGCTGGAGTGAGGACAGCCGCCCTTACTTGTTTCAGCTGCTCCAGCGC
CTAGAAGCTGCTTCTAGATCTGCCGATGACAAGGCTGTGTTGCAAGTGCCAGAGTTGGTG
GTGCCTGAACTGTATGCAGATGTGGCTGGCATCAGGGCAGAAAGCATTTTCTATAGCTTC
AGTGTCCTTTGAAGATGGTCTTAGACAAATGACTATATATGGGTGGAATTAGTTCCCTTCA
AGAACAGAGAGAAGGAACTTTCTGTGGCCACCAAGGGAGAAAAAAGGACATGGATCTTG
CATCTTTCCCTAAACATTTTCTTAGACATCTGAAATGCTGCTGGATGAAGCTCTACCTCT
ACATACCATGTACTCTTGAGCTAAGAATCACCATCAATTGTAGTTTGCTTTCCAGTCCCA
AGGGCTGAAGTATAAGTGGTGGACCGTGTCATTCTAAAGGAGGTTTTTAAATCTGCAAT
GATTGTAAGGGAATTAGGCAAAAGGGCTGGTCCCCTCACTCCAGGCTGGTTTACTACTG
AAACTAGTTTTTCTTTTCTTTTTTTTTTAAAGTTAAACTATTACAGAGTAAAAATAAACCAG
ATGGGCATGAATGAACACCTTCTAATTTTTTAACCATGAATTGAATATTGGAATTCATGAG
AAAGAAAATTCTAGGTTCTTTTTTGCTAAGAGGTGTTAAGGTGAGTCAATATATCCTTCAA
GGAAAGGCTTTGTCTCATCTATGTTGACGGGACGTAAAGTCCTCGTCCCGTTATGAAGA
GCTGAAGAAGATCTATAAGAAACAATACTGAGCCTTTCTTGACTATAGATAGAAGAGCA
TCCTTTTCAATTGAACCTCTGAGGCAGGTGGACCATGCATGATACTAAGTTTAAATTAGAAGCA
GGAGGAGTCATTTTCATGATTAGGAACATTGTTTCATCCCATTTGTTTGCCAGTTCCCTGTAA
GACTAAGGAGAATCAGCCTATAGAGCCAAAGCTAGAACCAGGGATAAAAAGTGTGTGTGT
GTATAACAAATAGGAAGCATGAAAGTCGAGCAAGAAGACTTAGTAACCCAGGTGGTCATT
AAGAGGTACAGAGAAGAAGTAATCTTATAGGAATGGATGGTAGCTTCTAATTTTTTAACCA
TTCATTGAAATAACTGTGAAGCAACTCATTAACCTAGTATTTATTGACCAAAAGTAGACT
TTTCAGGTGTATAGCTGCCAAAATCTCTATAATAAAGAGGCTAAAAGAAAATAAATGGGA
GTTATTTTACTAGGAAAATTAGAGAACCTATAGTTTCCAAAAGAGATTCTTTATGTGCA
AAATGAGATAACTCTCTACCTCACAGGGTTGGTGTGAGGAACAATGAGAATATGTATTTG
TGTATTATGTAGAATATAATATATTCTCAATAAATACTAGTTTTTCCCCTTTC

SEQ ID NO: 118_SGK2ALPHA_H

GAAGAGGGCAGAGCCGTGCATGGGGCTGCTCCCCAGGACCTGAGCAGGAACCTGGAGTTT
TCAGAGCTGCCTGATCATTGCTACAGAATGAACTCTAGCCCAGCTGGGACCCCAAGTCCA
CAGCCCTCCAGGGCCAATGGGAACATCAACCTGGGGCCTTCAGCCAACCCAAATGCCCAG
CCCACGGACTTCGACTTCTCAAAGTCATCGGCAAAGGGAACCTACGGGAAGGTCTACTG
GCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGTGAAGGTACTACAGAAAAAGTCCATC
TTAAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAACGTG
CGGCACCCCTTCTCGTGGGCCTGCGCTACTCCTTCCAGACACCTGAGAAGCTCTACTTC
GTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCCGTTTC
CTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGTGGCCAGCGCCATTGGCTACCTGCAC
TCCCTCAACATCATTTACAGGGATCTGAAACCAGAGAACATTCTCTTGACTGCCAGGGA
CACGTGGTGTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA

FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT
GATCGAGCAGTGGACTGGTGGTGCTTGGGGGCAGTCCTCTACGAGATGCTCCATGGCCTG
CCGCCCTTCTACAGCCAAGATGTATCCCAGATGTATGAGAACATTCTGCACCAGCCGCTA
CAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGACCTCCTGCAAAGCCTTCTCCACAAG
GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTG
TCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCA
TTCCTGGGATTTTCTTATGCGCCAGAGGATGATGACATCTTGGATTGCTAGAAGAGAAGG
ACCTGTGAACTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGCTAGGAA
GAGCGACTCAAAC TAACAATGGCTTCAACGAGAAGCAGGTTTATTTTTTCCAGCACATAA
AAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC
TGATCTCTGCCCTGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTGCTACAAGATG
GTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGA
GAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAGCTCCCCCAATGACTTTTGCTT
CCATCTCACTAACCACCCACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCTTATTTGC
TGGGTACGTGACTATCCCTAATAACAAAGGGGTTTTGACCCTAAGACATTAGGGGAGAAT
GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTTTGATTTTGATCT
CAATGTGTAAATGACAGAGATGTAACAAGCTCATAGGGTATCAATATCTCTTATTGTTT
TATGTTGAAAAA

SEQ ID NO: 120_CCRK_H

ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGGCGCCACGGCATCGTCTTCAAG
GCCAAGCACGTGGAGACTGGCGAGATAATTGCCCTCAAGAAGGTGGCCCTAAGGCGGTTG
GAAGACGGCTTCCCTAACCAGGCCCTGCGGGAGATTAAGGCTCTGCAGGAGATGGAGGAC
AATCAGTATGTGGTACAACCTGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCC
TTTGAGTTCATGCTGTGCGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGCC
CAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCGCTTCTGCCATGCC
AACAAACATTGTACATCGGGACCTGAAACCTGCCAACCTGCTCATCAGCGCCTCAGGCCAG
CTCAAGATAGCGGACTTTGGCCTGGCTCGAGTCTTTTCCCCAGACGGCAGCCGCCTCTAC
ACACACCAGGTGGCCACCAGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGGGTCC
CCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGCTTCGCATCTTGGGC
ACCCCAAACCTCAAGTCTGGCCGGAGCTCACTGAGCTGCCGGACTACAACAAGATCTCC
TTTAAGGAGCAGGTGCCCATGCCCCTGGAGGAGGTGCTGCCTGACGTCTCTCCCAGGCA
TTGGATCTGCTGGGTCAATTCCTTCTCTACCCTCCTCACCAGCGCATCGCAGCTTCCAAG
GCTCTCCTCCATCAGTACTTCTTACAGCTCCCCTGCCTGCCCATCCATCTGAGCTGCCG
ATTCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGCCCCCCCCACATCCAT
GACTTCCACGTGGACCGGCCTCTTGAGGGAGTCGCTGTTGAACCCAGAGCTGATTCGGCC
CTTCATCCTGGAGGGGTGAGAAGTTGGCCCTGGTCCCGTCTGCCTGCTCCTCAGGACCAC
TCAGTCCACCTGTTCTCTGCCACCTGCCTGGCTTCACCCTCCAAGGCCTCCCCATGGCC
ACAGTGGGCCCCACACCACACCTTGCCCTTAGCCCTTGCGAGGGTTGGTCTCGAGGCAGA
GGTCATGTTCCCAGCCAAGAGTATGAGAACATCCAGTCGAGCAGAGGAGATTTCATGGCCT
GTGCTCGGTGAGCCTTACCTTCTGTGTGCTACTGACGTACCCATCAGGACAGTGAGCTCT
GCTGCCAGTCAAGGCCTGCATATGCAGAAATGACGATGCCTGCCTTGGTGCTGCTTCCCC
GAGTGCTGCCTCCTGGTCAAGGAGAAGTGACAGAGAGTAA

SEQ ID NO: 121_TESK2_H

GAATTCGCGGCCGCTCGACGCTCAGCAGAGCTACCAGCTGCCCTGTTGGCTTCGCTGGTC
GGATCGTCTCCTGGCCCCGCCAAACAGGCGAGCGGCCCGACTGTGGGGCATGGCAGTA
GTCTCCTCGTTCTCCGCCGCCGCTAGCCTAGCTGAGTCGCCGGCTTCTGCGCTAGGGGCT

FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC
TCCCTCTTTGCCGCCGTCTCCTCCTCTTGCCCGCGCAGGCACCCCTCTGGCTGCTCAGTC
CTGCCTCAGTGTCAAACCAGAAGAGAAGTAAAATTCAACAAAAATTTATGTGTGGAGTTC
CTTCTTAAAGAAGAAAAAAGTGATTATTTAGACTATGGATCGGAGCAAACGGAATTCAA
TTGCAGGATTTCCCTCCACGTGTGGAGCGTCTTGAAGAGTTTGAAGGAGGTGGTGGAGGAG
AAGGAAATGTGAGCCAGGTGGGAAGAGTTTGGCCATCTTCGTATCGAGCTCTTATAAGTG
CCTTTTCCAGACTGACGCGTTTGGATGATTTACCTGTGAAAAAATAGGGTCTGGCTTCT
TTTCTGAAGTGTTCAAGGTACGACACCGAGCTTCTGGTCAGGTGATGGCTCTTAAGATGA
ACACATTGAGCAGTAACCGGGCAAACATGCTGAAAGAAGTACAGCTCATGAATAGACTCT
CCCATCCCAACATCCTTAGGTATATCAACTCCGGGAACCTGGAACAGTTGCTAGACAGTA
ACCTGCATTTGCCTTGGACTGTGAGGGTAAACTGGCCTATGACATAGCAGTGGGCCTCA
GCTACCTTCACTTCAAAGGCATTTTTTCATCGGGACCTCACATCTAAGAACTGCCTGATAA
AGAGGGATGAGAATGGTTACTCTGCAGTGGTAGCTGACTTTGGCCTGGCTGAGAAGATCC
CCGATGTCAGCATGGGGAGTGAGAAGCTGGCCGTGGTGGGTTCCTTCTGGATGGCAC
CTGAGGTTCTCCGAGATGAGCCCTATAATGAAAAGGCAGATGTGTTCTCTTATGGTATCA
TCCTCTGCGAGATCATCGCCCGCATCCAGGCCGATCCGGACTATCTTCCCCCGCACAGAGA
ATTTCTGGGCTGGACTATGATGCTTTCCAGCACATGGTGGGAGACTGTCCCCCAGATTTTC
TGCAACTTACTTTCAACTGCTGTAACATGGATCCCAAACCTGCGCCCATCTTTTGTGGAGA
TTGGGAAGACCCTGGAGGAAATTCTGAGCCGCCTACAGGAAGAAGAGCAGGAGAGGGATA
GGAAGCTGCAGCCACAGCCAGGGGACTCTTGGAGAAAGCACCTGGGGTGAAGCGACTAA
GCTCACTGGATGACAAGATCCCCCACAAGTCACCATGCCCAAGACGTACCATCTGGCTGT
CTCGAAGCCAGTCAGATATCTTTTCCCGTAAGCCCCCACGTACAGTGAGTGTCTTGGACC
CATACTACCGGCCACGAGATGGTGCTGCCCGCACCCCCAAAGTCAACCCTTTTAGTGCTC
GCCAGGACCTCATGGGGGGCAAGATCAAGTTTTTTTGACCTGCCCAGCAAGTCTGTCTCT
CTCTGGTATTTGACCTGGATGCACCAGGGCCCGGAACCTATGCCCTGGCTGACTGGCAGG
AGCCCCCTGGCCCCACCTATTCGCCGGTGGCGTTCCTTGCCTGGTTCGCCTGAGTTCTTGC
ATCAAGAGGCTTGTCCATTTGTGGGCCGGGAAGAATCGCTATCTGATGGGCCCCCACCAC
GCCTAAGTAGTCTCAAGTACAGAGTTAAAGAGATCCCACCATTCCGGGCATCTGCCCTAC
CAGCTGCTCAAGCCCATGAGGCTATGGACTGCTCCATTCTCCAGGAAGAAAAATGGTTTTG
GGTCCAGGCCCCAGGGGACCAGTCCATGCCCTGCGGGTGCTTCTGAGGAGATGGAGGTAG
AAGAAAGGCCAGCAGGCTCAACTCCAGCCACCTTCTCCACCTCAGGCATAGGCCTGCAAA
CCCAGGGAAAGCAGGATGGGTGAGGGGGTTTAGTCCCTGCCTCACCTTGGGGATGGACCT
TCAGCTGAAACCATATGGCCCCCTAGGTGCACAGCCTTGATTCTTCCCTGGAGCCTACAG
AGCAGGCAGGCTAGGCCAAGCCAGGCTCAACTTCTGGGCTCCAGTGCCCATTTGGCTGTG
TATGACGGGAGGCAGCAGTGAGAGGCCTTCCTAGTTAGGGCCAACAGCTGATACCAAGCC
TCTGAAATCCAGCAAGGAGGTCTGCCTCCCACCAGACCCTCTCCAGTGTACTTCCCCAGA
TAGGACCAGAGGATGTCTAGTTCTAGGCTGAGCTGGCAGGCAGCTATTACCCCGGTTCTT
TCCCCACCCCAGGTCTGTCTCTTGCCTTTTCTTGGGGCATATAAGCTACTGAGTGGAACA
TGGAGCTGATCAAGAGGCCGTAATGGTCATGGCTGTTTCCAGACCTGAATATTGGGTGCT
TCTTGCCAGTATTCTAAGACATTTGAGTAATTGCTGTTTGCACCTTACTGCATGGTCAGAC
CACGTCACTACATTTCTATGCAAGGGGACAGCAAGGCAGCGTGGTGGTCATGGCTCTTAG
CTAACCTATTCAAAGACCTTTTCTGTGTTGATTAATCTATTTTCATATTTATAAAGGAGTC
TTAATGTTCTGCCCCATAAGACTTTCAACCTTGTGGTGGGAGTGGGGCTGGTTTTGTAG
GCCCTAGGGCCTGCTTCTATGTATTTATCAACATGTGATACATTCAATTGGTTAAATGGT
TTATACAGGGACTGATTTGCTTCCCTTCTGCCATGGCTGGAGCTTTGGGAACAGTCTGT
CCTTACAGAGCTGCAATAAGAAATAACCAAAGATGAAGCTGGTCAAATATTTTCATAACT
TGCTTCTGTTGATTTTTTTTTTTGTAAAACTTTCCCAAGACATTTTCAGACTTAAAAATAA
AGTCAGTGTTACAGGT

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
7 December 2000 (07.12.2000)

PCT

(10) International Publication Number
WO 00/73469 A3

(51) International Patent Classification⁷: C12N 15/54,
9/12, 15/11, 5/12, C07K 16/40, A61K 38/00, G01N 33/68

(74) Agent: FOLEY & LARDNER; Suite 500, 3000 K Street,
N.W., Washington, D.C. 20007-8696 (US).

(21) International Application Number: PCT/US00/14842

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE,
DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID,
IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL,
PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW.

(22) International Filing Date: 26 May 2000 (26.05.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/136,503 28 May 1999 (28.05.1999) US

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): SUGEN,
INC. [US/US]: 230 East Grand Avenue, South San Fran-
cisco, CA 94080 (US).

Published:

-- with international search report

(72) Inventors; and

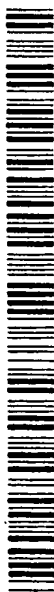
(75) Inventors/Applicants (*for US only*): PLOWMAN, Gre-
gory, D. [US/US]: 4 Honeysuckle Lane, San Carlos, CA
94070 (US). MARTINEZ, Ricardo [US/US]: 984 Cartier
Lane, Foster City, CA 94404 (US). WHYTE, David
[US/US]: 2623 Barclay Way, Belmont, CA 94002 (US).
SUDERSANAM, Sucha [US/US]: 20 Corte Patencio,
Greenbrae, CA 94904 (US).

(88) Date of publication of the international search report:
29 November 2001

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to kinase polypeptides, nucleotide sequences encoding the kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.



WO 00/73469 A3

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/14842

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/54 C12N9/12 C12N15/11 C12N5/12 C07K16/40
 A61K38/00 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, EMBL, MEDLINE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------|
| X | DATABASE EMBL 'Online! accession number W65887, 12 June 1996 (1996-06-12) MARRA M. ET AL.: "The WashU-HHMI mouse EST project." XP002157499 abstract DOC. AGAINST INV. 1 (SEQ.IDs. 122, 4) --- | 2,6,7, 11,12 |
| E | WO 00 58473 A (CURAGEN CORP.; LEACH MARTIN (US); SHIMKETS RICHARD A (US)) 5 October 2000 (2000-10-05) SEQ.IDs. 4435 and 4436 DOC. AGAINST INV. 1 (SEQ.IDs. 122, 4) SEQ.IDs. 5049, 5050, 5571, 5572 DOC. AGAINST INV. 67 (SEQ.IDs. 188, 70) SEQ.IDs. 3009 and 3010 DOC. AGAINST INV. 76 (SEQ.IDs. 197, 79) --- -/-- | 1,2,4-7, 11,12 |

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- *G* document member of the same patent family

Date of the actual completion of the international search

22 June 2001

Date of mailing of the international search report

18. 07. 2001

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
 NL - 2280 HV Rijswijk
 Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
 Fax: (+31-70) 340-3016

Authorized officer

Mandl, B

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|---------------------------------------|
| P,X | <p>RUIZ-PEREZ V. L. ET AL.: "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers acrodistal dysostosis." NATURE GENETICS, vol. 24, no. 3, March 2000 (2000-03), pages 283-286, XP002157498 ISSN: 1061-4036 page 284, left-hand column, line 6 - line 8 figure 1A page 286, right-hand column, last paragraph & DATABASE EMBL 'Online! Accession Number Q9NY57, 1 October 2000 (2000-10-01) RUIZ-PEREZ V. V. ET AL.: "Serine/threonine protein kinase." abstract DOC. AGAINST INV. 1 (SEQ.IDs. 122, 4)</p> | 1-12 |
| X | <p>DATABASE EMBL 'Online! Accession Number AA305176, 18 April 1997 (1997-04-18) ADAMS M. D. ET AL.: "EST176172 colon carcinoma cell line II Homo sapiens cDNA 5'-end." XP002165842 abstract DOC. AGAINST INV. 3 (SEQ.IDs. 124, 6)</p> | 6,7 |
| X | <p>DATABASE EMBL 'Online! Accession Number AA116841, 16 November 1996 (1996-11-16) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:538568 5' similar to TR:G406058 protein kinase." XP002165843 abstract DOC. AGAINST INV. 4 (SEQ.IDs. 125, 7)</p> | 1,2,4,6, 7,10-13, 15 |
| P,X | <p>WO 00 06728 A (INCYTE PHARMA INC ; PATTERSON CHANDRA (US); AZIMZAI YALDA (US); COR) 10 February 2000 (2000-02-10) SEQ.ID.1 and 32 DOC. AGAINST INV. 4 (SEQ.IDs. 125, 7)</p> | 2,4-7,9, 11-14, 26,27, 35,36 |
| X | <p>WO 98 58052 A (INCYTE PHARMA INC ; CORLEY NEIL C (US); BANDMAN OLGA (US); GOLI SUR) 23 December 1998 (1998-12-23) SEQ.IDs. 4 and 11 DOC. AGAINST INV. 5 (SEQ.IDs. 126, 8)</p> | 1-14, 26-30, 35-38 |
| | -/-- | |

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|----------------------------|
| E | WO 00 55332 A (INCYTE PHARMA INC ;AZIMZAI YALDA (US); YUE HENRY (US); AU YOUNG JA) 21 September 2000 (2000-09-21) SEQ.IDs. 7 and 21 DOC. AGAINST INV. 6 (SEQ.IDs. 127, 9) SEQ.IDs. 2 and 16 DOC. AGAINST INV. 26 (SEQ.IDs. 147, 29) --- | 1-15, 26-30, 35-38 |
| X | DATABASE EMBL 'Online! Accession Number AA593989, 24 September 1997 (1997-09-24) STRAUSBERG R.: "Homo sapiens clone IMAGE:1084047 3' similar to TR:G20878 serine/threonine protein kinase." XP002165844 abstract DOC. AGAINST INV. 6 (SEQ.IDs. 127, 9) --- | 1,2,4,6, 7,10-13, 15 |
| X | DATABASE EMBL 'Online! Accession Number AL050147, 20 May 1999 (1999-05-20) WAMBUTT R. ET AL.: "Homo sapiens mRNA." XP002165845 abstract DOC. AGAINST INV. 6 (SEQ.IDs. 127, 9) --- | 6,7 |
| X | HAYASHI A. ET AL.: "PKCnu, a new member of the protein kinase C family, composes a fourth subfamily with PKCmu." BIOCHIMICA ET BIOPHYSICA ACTA, vol. 1450, no. 1, 6 May 1999 (1999-05-06), pages 99-106, XP000992627 ISSN: 0006-3002 the whole document DOC. AGAINST INV. 8 (SEQ.IDs. 129, 11) --- | 1-15, 35-38 |
| X | DATABASE EMBL 'Online! Accession Number AA763046, 28 January 1998 (1998-01-28) MARRA M. ET AL.: "Mus musculus cDNA clone similar to TR:P70268 protein kinase." XP002165846 abstract DOC. AGAINST INV. 9 (SEQ.IDs. 130, 12) --- | 2,6,7, 11,12 |
| | --- -/-- | |

INTERNATIONAL SEARCH REPORT

Int .tional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|---|
| P,X | OISHI K. ET AL.: "Identification and characterization of PKNbeta, a novel isoform of protein kinase PKN: Expression and arachidonic acid dependency are different from those of PKNalpha." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 261, no. 3, 11 August 1999 (1999-08-11), pages 808-814, XP002165839 ISSN: 0006-291X figure 1 DOC. AGAINST INV. 9 (SEQ.IDs. 130, 12) | 1-15,26, 27,35,37 |
| X | DATABASE EMBL 'Online! Accession Number H19102, 2 July 1995 (1995-07-02) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:171993 5' similar to SP:F31E3.2 CE01267 protein kinase." XP002165847 abstract DOC. AGAINST INV. 11 (SEQ.IDs. 132, 14) | 2,6,7, 11,12 |
| X | WO 97 33909 A (CORIXA CORP) 18 September 1997 (1997-09-18) SEQ.IDs.6 and 16 DOC. AGAINST INV. 12 (SEQ.IDs. 133, 15) | 2,6,7,9, 11,12, 26,27, 35-38 |
| X | DATABASE EMBL 'Online! Accession Number AA463334, 13 June 1997 (1997-06-13) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:811660 5' similar to SW:COT1_NEUCR P38679 serine/threonine-protein kinase COT-1." XP002165848 abstract DOC. AGAINST INV. 12 (SEQ.IDs. 133, 15) | 1,2,4,6, 7,10-13, 15 |
| P,X | WO 99 57144 A (INCYTE PHARMA INC ;PATTERSON CHANDRA (US); AZIMZAI YALDA (US); RED) 11 November 1999 (1999-11-11) SEQ.IDs. 52 and 117 DOC. AGAINST INV. 12 (SEQ.IDs. 133, 15) -/-- | 2,6,7,9, 11,12, 26,27, 29,30, 35-38 |

INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------|
| P,X | ZHANG H. ET AL.: "Cloning, characterization, and chromosome mapping of RPS6KC1, a novel putative member of the ribosome protein S6 kinase family, to chromosome 12q12-q13.1." GENOMICS, vol. 61, no. 3, 1 November 1999 (1999-11-01), pages 314-318, XP002165840 ISSN: 0888-7543 the whole document DOC. AGAINST INV. 12 (SEQ.IDs. 133, 15) | 1-15,35 |
| X | DATABASE EMBL 'Online! Accession Number AC006530, 8 February 1999 (1999-02-08) ROWEN L. ET AL.: "Sequencing of human chromosome 14." XP002165849 abstract DOC. AGAINST INV. 14 (SEQ.IDs. 135, 17) | 1,2,4-7, 10-15 |
| X | DATABASE EMBL 'Online! Accession Number AI215680, 23 October 1998 (1998-10-23) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:1884219." XP002165850 abstract DOC. AGAINST INV. 14 (SEQ.IDs. 135, 17) | 6,7 |
| X | WO 98 11234 A (HAWKINS PHILLIP R ;INCYTE PHARMA INC (US); AU YOUNG JANICE (US); G) 19 March 1998 (1998-03-19) SEQ.IDs. 5 and 6 DOC. AGAINST INV. 15 (SEQ.IDs. 136, 18) DOC. AGAINST INV. 16 (SEQ.IDs. 137, 19) | 1-15, 26-30, 35-38 |
| X | EP 0 861 896 A (DADE BEHRING MARBURG GMBH) 2 September 1998 (1998-09-02) SEQ.IDs. 1 and 2 DOC. AGAINST INV. 15 (SEQ.IDs. 136, 18) DOC. AGAINST INV. 16 (SEQ.IDs. 137, 19) | 1-15, 26-28, 35-38 |
| P,X | DATABASE EMBL 'Online! Accession Number AF205855, 23 December 1999 (1999-12-23) SHIGAIEV A. ET AL.: "Mus musculus serum and glucocorticoid-dependent protein kinase (Sgk) mRNA." XP002165851 abstract DOC. AGAINST INV. 16 (SEQ.IDs. 137, 19) | 1,2,4,6, 7,10-13, 15 |
| | -/-- | |

INTERNATIONAL SEARCH REPORT

Int ional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|--------------------------------|
| E | WO 00 35946 A (UNIV DUNDEE ;COHEN PHILIP (GB); DEAK MARIA (GB); KOBAYASHI TAKAYAS) 22 June 2000 (2000-06-22) figure 11 DOC. AGAINST INV. 17 (SEQ.IDs. 138, 20) DOC. AGAINST INV. 113 (SEQ.IDs. 234, 116) --- | 1-14, 26, 27, 29, 30 |
| X | DATABASE EMBL 'Online! Accession Number Z98752, 23 August 1997 (1997-08-23) RAMSAY H.: "Human DNA sequence from clone RP1-13887 on chromosome 20q13.12." XP002165852 abstract DOC. AGAINST INV. 17 (SEQ.IDs. 138, 20) --- | 1-14 |
| X | WO 98 31802 A (GENETICS INST) 23 July 1998 (1998-07-23) SEQ.IDs. 13 and 14 DOC. AGAINST INV. 21 (SEQ.IDs. 142, 24) --- | 6, 7, 11, 12 |
| X | DATABASE EMBL 'Online! Accession Number A1061003, 23 July 1998 (1998-07-23) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:1379597 5' similar to TR:008875 calcium calmodulin dependent kinase CPG16." XP002165853 abstract DOC. AGAINST INV. 22 (SEQ.IDs. 143, 25) --- | 1, 2, 4, 6, 7, 10-13, 25 |
| X | DATABASE EMBL 'Online! Accession Number AA383293, 18 April 1997 (1997-04-18) ADAMS M. D. ET AL.: "Homo sapiens cDNA 5'-end similar to serine/threonine kinase p78." XP002165854 abstract DOC. AGAINST INV. 23 (SEQ.IDs. 144, 26) --- | 1, 2, 4, 6, 7, 10-13, 16 |
| X | DATABASE EMBL 'Online! Accession number AA197883, 29 January 1997 (1997-01-29) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:654045 5' similar to TR:G406113 protein kinase I." XP002165855 abstract DOC. AGAINST INV. 24 (SEQ.IDs. 145, 27) --- | 1, 2, 4, 6, 7, 10-13 |
| | --- -/-- | |

INTERNATIONAL SEARCH REPORT

Int .tional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|---------------------------------------|
| P, X | WO 99 50395 A (HELIX RESEARCH INST ;MURAMATSU MASAOKI (JP); TOKUMITSU HIROSHI (JP) 7 October 1999 (1999-10-07) page 41 -page 51 DOC. AGAINST INV. 24 (SEQ.IDs. 145, 27) ---- | 1-4,6-13 |
| X | SANJO H. ET AL: "DRAKs, novel serine/threonine kinases related to death-associated protein kinase that trigger apoptosis." JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 44, 30 October 1998 (1998-10-30), pages 29066-29071, XP002165841 ISSN: 0021-9258 figure 1 DOC. AGAINST INV. 26 (SEQ.IDs. 147, 29) ---- | 1-14,16, 35,37 |
| P, X | WO 99 33961 A (AKIRA SHIZUO ;KAWAI TARO (JP); ASAHI CHEMICAL IND (JP)) 8 July 1999 (1999-07-08) SEQ.IDs. 5 and 6 DOC. AGAINST INV. 26 (SEQ.IDs. 147, 29) SEQ.IDs. 29 and 30 DOC. AGAINST INV. 40 (SEQ.IDs. 161, 43) ---- | 1-14,16, 26,27, 29,30, 35,37 |
| X | NAGASE T. ET AL.: "PREDICTION OF THE CODING SEQUENCE OF UNIDENTIFIED HUMAN GENES. XIII. THE COMPLETE SEQUENCE OF 100 NEW CDNA CLONES FROM BRAIN WHICH CODE FOR LARGE PROTEINS IN VITRO" DNA RESEARCH, vol. 6, 26 February 1999 (1999-02-26), pages 63-70, XP000952912 ISSN: 1340-2838 the whole document -& DATABASE EMBL 'Online! Accession Number AB023153, 9 April 1999 (1999-04-09) NAGASE T. ET AL.: "Homo sapiens mRNA for KIAA0936 protein." XP002166242 abstract DOC. AGAINST INV. 54 (SEQ.IDs. 175, 57) -& DATABASE EMBL 'Online! Accession Number AB023216, 9 April 1999 (1999-04-09) NAGASE T. ET AL.: "Homo sapiens mRNA for KIAA0999 protein." XP002166243 abstract DOC. AGAINST INV. 28 (SEQ.IDs. 149, 31) ----- -/-- | 1,2,4-7, 10-14, 16,19 |

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No |
|------------|--|---|
| X | <p>WO 98 01756 A (UNIV WASHINGTON) 15 January 1998 (1998-01-15)</p> <p>SEQ.IDs. 1 and 2 DOC. AGAINST INV. 30 (SEQ.IDs. 151, 33)</p> <p style="text-align: center;">---</p> | <p>1-14, 16, 26, 27, 35, 36</p> |
| X | <p>DATABASE EMBL 'Online! Accession Number W90839, 9 July 1996 (1996-07-09) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:420441 5' similar to gb:M80359 putative serine/threonine protein kinase." XP002165856 abstract DOC. AGAINST INV. 31 (SEQ.IDs. 152, 34)</p> <p style="text-align: center;">---</p> | <p>1, 2, 4, 6, 7, 10-13, 16</p> |
| X | <p>NAGASE T. ET AL.: "PREDICTION OF THE CODING SEQUENCES OF UNIDENTIFIED HUMAN GENES. IV. THE CODING SEQUENCES OF 40 NEW GENES (KIAA0121-KIAA0160) DEDUCED BY ANALYSIS OF CDNA CLONES FROM HUMAN CELL LINE KG-1" DNA RESEARCH, vol. 2, no. 4, 31 August 1995 (1995-08-31), pages 167-174, XP000676653 ISSN: 1340-2838 the whole document -& DATABASE EMBL 'Online! Accession Number D50925, 1 August 1996 (1996-08-01) NAGASE T. ET AL.: "Human mRNA for KIAA0135 gene." XP002166244 abstract DOC. AGAINST INV. 32 (SEQ.IDs. 153, 35) DOC. AGAINST INV. 33 (SEQ.IDs. 154, 36)</p> <p style="text-align: center;">---</p> | <p>1, 2, 4-7, 10-14, 16</p> |
| X | <p>DATABASE EMBL 'Online! Accession Number U79240, 14 December 1996 (1996-12-14) YU W. ET AL.: "Human serine/threonine kinase mRNA." XP002165857 abstract DOC. AGAINST INV. 33 (SEQ.IDs. 154, 36)</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p> | <p>1, 2, 4-7, 10-14</p> |

INTERNATIONAL SEARCH REPORT

Int ional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|----------------------------|
| X | <p>DATABASE EMBL 'Online! Accession Number AI036899, 29 June 1998 (1998-06-29) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:1746011 5' similar to TR:Q99763 serine/threonine protein kinase." XP002165858 abstract DOC. AGAINST INV. 33 (SEQ.IDs. 154, 36)</p> | 1,2,4,6, 7,10-13 |
| X | <p>DATABASE EMBL 'Online! Accession Number AI469033, 17 March 1999 (1999-03-17) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2137322." XP002165859 abstract DOC. AGAINST INV. 35 (SEQ.IDs. 156, 38)</p> | 6,7 |
| X | <p>DATABASE EMBL 'Online! Accession Number AC007225, 7 April 1999 (1999-04-07) BRUCE D. ET AL.: "Homo sapiens chromosome 16 clone RPCI-11_480G7." XP002166245 abstract DOC. AGAINST INV. 37 (SEQ.IDs. 158, 40)</p> | 6,7 |
| P,X | <p>WO 99 49062 A (FAN WUFANG ; GENE LOGIC INC (US); PRASHAR YATINDRA (US)) 30 September 1999 (1999-09-30) SEQ.IDs. 1 and 2 DOC. AGAINST INV. 37 (SEQ.IDs. 158, 40) DOC. AGAINST INV. 55 (SEQ.IDs. 176, 58)</p> | 1-14, 26-30, 35-38 |
| X | <p>DATABASE EMBL 'Online! Accession Number AI596766, 26 April 1999 (1999-04-26) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:949322 5' similar to WP:ZC373.4 CE02377 myosin-light-chain kinase domain." XP002166246 abstract DOC. AGAINST INV. 38 (SEQ.IDs. 159, 41) DOC. AGAINST INV. 39 (SEQ.IDs. 160, 42)</p> | 1,2,4,6, 7,10-13, 16 |

-/--

INTERNATIONAL SEARCH REPORT

Int ional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------------|
| P, X | <p>NAGASE T. ET AL.: "PREDICTION OF THE CODING SEQUENCES OF UNIDENTIFIED HUMAN GENES. XVI. THE COMPLETE SEQUENCES OF 150 NEW CDNA CLONES FROM BRAIN WHICH CODE FOR LARGE PROTEINS IN VITRO"</p> <p>DNA RESEARCH, vol. 7, 28 February 2000 (2000-02-28), pages 65-73, XP000923011 KIAA1297 -& DATABASE EMBL 'Online! Accession Number AB037718, 14 March 2000 (2000-03-14) OHARA O. ET AL.: "Homo sapiens mRNA for KIAA1297 protein." XP002166247 abstract DOC. AGAINST INV. 38 (SEQ.IDs. 159, 41) DOC. AGAINST INV. 39 (SEQ.IDs. 160, 42) -& DATABASE EMBL 'Online! Accession Number AB037759, 14 March 2000 (2000-03-14) OHARA O. ET AL.: "Homo sapiens mRNA for KIAA1338 protein." XP002167889 abstract DOC. AGAINST INV. 67 (SEQ.IDs. 188, 70) -& DATABASE EMBL 'Online! Accession Number AB037790, 14 March 2000 (2000-03-14) OHARA O. ET AL.: "Homo sapiens mRNA for KIAA1369 protein." XP002167890 abstract DOC. AGAINST INV. 68 (SEQ.IDs. 189, 71) -& DATABASE EMBL 'Online! Accession Number AB037781, 14 March 2000 (2000-03-14) NAGASE T. ET AL.: "Homo sapiens mRNA for KIAA1360 protein, partial cds." XP002168226 abstract DOC. AGAINST INV. 82 (SEQ.IDs. 203, 85)</p> | 1,2,4-7, 10-14, 16,25 |
| X | <p>KAWAI T. ET AL.: "Duet is a novel serine/threonine kinase with Dbl-Homology (DH) and Pleckstrin-Homology (PH) domains"</p> <p>GENE, vol. 227, no. 2, 18 February 1999 (1999-02-18), pages 249-255, XP004158739 ISSN: 0378-1119 the whole document DOC. AGAINST INV. 40 (SEQ.IDs. 161, 43)</p> <p style="text-align: center;">-/--</p> | 1-14,29, 30,35-38 |

INTERNATIONAL SEARCH REPORT

Int .tional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|----------------------------|
| X | <p>DATABASE EMBL 'Online! Accession Number AA454060, 11 June 1997 (1997-06-11) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:795492 5' similar to TR:G49075 calmodulin-binding protein." XP002166248 abstract DOC. AGAINST INV. 41 (SEQ.IDs. 162, 44)</p> | 6,7 |
| X | <p>DATABASE EMBL 'Online! Accession Number AI385971, 29 January 1999 (1999-01-29) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:514336 5' similar to WP:R90.1 CE06325 protein kinase." XP002166249 abstract DOC. AGAINST INV. 43 (SEQ.IDs. 164, 46)</p> | 1,2,4,6, 7,10-13, 16 |
| X | <p>DATABASE EMBL 'Online! Accession Number AA436054, 1 June 1997 (1997-06-01) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:730582 5' similar to gb:X66363 serine/threonine-protein kinase pctaie-1" XP002166250 abstract DOC. AGAINST INV. 44 (SEQ.IDs. 165, 47)</p> | 1,2,4-7, 10-14,16 |
| X | <p>DATABASE EMBL 'Online! Accession Number AA061797, 24 September 1996 (1996-09-24) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:513953 5' similar to gb:X66358 serine/threonine-protein kinase." XP002166251 abstract DOC. AGAINST INV. 45 (SEQ.IDs. 166, 48) DOC. AGAINST INV. 46 (SEQ.IDs. 167, 49)</p> | 1,2,4,6, 7,10-13, 17 |
| A | <p>WO 98 35015 A (GERHOLD DAVID L ;MERCK & CO INC (US)) 13 August 1998 (1998-08-13) SEQ.IDs.2 and 3 DOC. AGAINST INV. 50 (SEQ.IDs. 171, 53) DOC. AGAINST INV. 114 (SEQ.IDs. 235, 117)</p> | 1-30, 35-38 |
| | <p>----- -/--</p> | |

INTERNATIONAL SEARCH REPORT

Int. Patent Application No.

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|----------|--|--------------------------------|
| X | NAYLER O. ET AL.: "Characterization and comparison of four serine- and arginine-rich (SR) protein kinases." BIOCHEMICAL JOURNAL, vol. 326, no. 3, 1997, pages 693-700, XP002166240 ISSN: 0264-6021 the whole document DOC. AGAINST INV. 51 (SEQ.IDs. 172, 54) --- | 1-4, 6-13, 18, 26, 27 |
| P, X | WO 99 38981 A (AKERBLOM INGRID E ; INCYTE PHARMA INC (US); CORLEY NEIL C (US); BAN) 5 August 1999 (1999-08-05) SEQ.IDs. 3 and 9 DOC. AGAINST INV. 51 (SEQ.IDs. 172, 54) SEQ.IDs. 6 and 12 DOC. AGAINST INV. 95 (SEQ.IDs. 216, 43) --- | 1-14, 18, 26-30, 35-38 |
| X | DATABASE EMBL 'Online! Accession Number AA839940, 2 March 1998 (1998-03-02) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:1259911 5' similar to SW:KMLC_RAT P20689 myosin light chain kinase." XP002167891 abstract DOC. AGAINST INV. 55 (SEQ.IDs. 176, 58) --- | 1, 2, 4, 6, 7, 10-13, 18 |
| X | DATABASE EMBL 'Online! Accession Number AL031055, 10 July 1998 (1998-07-10) RAMSAY H.: "Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1." XP002167892 abstract DOC. AGAINST INV. 56 (SEQ.IDs. 177, 59) --- | 1, 2, 4-7, 10-14, 18 |
| P, X | DATABASE EMBL 'Online! Accession Number AL137662, 27 January 2000 (2000-01-27) KOEHRER K. ET AL.: "Homo sapiens mRNA" XP002167893 abstract DOC. AGAINST INV. 57 (SEQ.IDs. 178, 60) --- | 2, 6, 7, 11, 12 |
| | --- -/-- | |

INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------------|
| X | <p>NAGASE T. ET AL.: "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro"</p> <p>DNA RESEARCH, vol. 4, no. 4, 28 April 1997 (1997-04-28), pages 141-150, XP002102085 ISSN: 1340-2838 the whole document -& DATABASE EMBL 'Online! Accession Number AB002342, 1 July 1997 (1997-07-01) NAGASE T. ET AL.: "Human mRNA for KIAA0344 gene." XP002167894 abstract DOC. AGAINST INV. 59 (SEQ.IDs. 180, 62)</p> | 2,6,7, 11,12 |
| X | <p>WO 98 36054 A (HOOPER JOHN DAVID ;AMRAD OPERATIONS PTY LTD (AU); ANTALIS TONI MAR) 20 August 1998 (1998-08-20) SEQ.IDs. 9 and 10 DOC. AGAINST INV. 60 (SEQ.IDs. 181, 63)</p> | 1-14, 26-30, 35-38 |
| X | <p>ANDERSON K. A. ET AL.: "Components of a calmodulin-dependent protein kinase cascade. Molecular cloning, functional characterization and cellular localization of Ca²⁺/calmodulin-dependent protein kinase kinase beta."</p> <p>JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 48, 27 November 1998 (1998-11-27), pages 31880-31889, XP002167887 ISSN: 0021-9258 the whole document -& DATABASE EMBL 'Online! Accession Number AF140507, 21 May 1999 (1999-05-21) ANDERSON K. A. ET AL.: "Homo sapiens Ca²⁺/calmodulin-dependent protein kinase beta, complete cds." XP002167895 abstract DOC. AGAINST INV. 62 (SEQ.IDs. 183, 65)</p> | 1-14,23, 26,27 |
| P,X | <p>WO 99 58558 A (INCYTE PHARMA INC ;PATTERSON CHANDRA (US); YUE HENRY (US); BANDMAN) 18 November 1999 (1999-11-18) SEQ.IDs. 2 and 15 DOC. AGAINST INV. 62 (SEQ.IDs. 183, 65)</p> <p style="text-align: center;">-/--</p> | 2,6,7,9, 11,12, 26-28 |

INTERNATIONAL SEARCH REPORT

Int ional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|----------------------------|
| X | DATABASE EMBL 'Online! Accession Number AC004685, 15 May 1998 (1998-05-15) ADAMS M. D. AND LOFTUS B. J.: "Homo sapiens chromosome 16 BAC clone CIT987SK-A-233A8." XP002167896 abstract DOC. AGAINST INV. 63 (SEQ.IDs. 184, 66) --- | 1,2,4-7 |
| P,X | US 6 013 455 A (AZIMZAI YALDA ET AL) 11 January 2000 (2000-01-11) SEQ.IDs. 2 and 11 DOC. AGAINST INV. 63 (SEQ.IDs. 184, 66) --- | 1-14, 26-30, 35-38 |
| X | EP 0 870 825 A (SMITHKLINE BEECHAM CORP) 14 October 1998 (1998-10-14) figure 2 DOC. AGAINST INV. 65 (SEQ.IDs. 186, 68) DOC. AGAINST INV. 66 (SEQ.IDs. 187, 69) --- | 1-14, 25-30, 35-38 |
| X | DATABASE EMBL 'Online! Accession Number AA589241, 18 September 1997 (1997-09-18) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:992145 5' similar to WP:F49E11.1 CE05897 serine/threonine protein kinase." XP002167897 abstract DOC. AGAINST INV. 66 (SEQ.IDs. 187, 69) --- | 1,2,4,6, 7,10-13, 25 |
| P,X | BERLANGA J. J. ET AL.: "Characterization of a mammalian homolog of the GCN2 eukaryotic initiation factor 2alpha kinase." EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 265, no. 2, October 1999 (1999-10), pages 754-762, XP002167888 ISSN: 0014-2956 the whole document DOC. AGAINST INV. 67 (SEQ.IDs. 188, 70) --- | 1-14, 25-27,35 |
| X | WO 94 05794 A (MASSACHUSETTS INST TECHNOLOGY) 17 March 1994 (1994-03-17) page 13, paragraph 2 examples 1,2 DOC. AGAINST INV. 68 (SEQ.IDs. 189, 71) --- | 1-14, 26-28, 35-38 |
| | --- -/-- | |

INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|---------------------------------------|
| X | MELLOR H. ET AL.: "CLONING AND CHARACTERIZATION OF CDNA ENCODING RAT HEMIN-SENSITIVE INITIATION FACTOR-2ALPHA (EIF-2ALPHA) KINASE" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 269, no. 14, 8 April 1994 (1994-04-08), pages 10201-10204, XP002920790 ISSN: 0021-9258 the whole document DOC. AGAINST INV. 68 (SEQ.IDs. 189, 71) --- | 1-4,6-13 |
| X | DATABASE EMBL 'Online! Accession Number AA387681, 25 June 1997 (1997-06-25) MARRA M. ET AL.: "Mus musculus cDNA clone." XP002167898 abstract DOC. AGAINST INV. 70 (SEQ.IDs. 191, 73) --- | 6,7 |
| P,X | WO 00 09678 A (TULARIK INC) 24 February 2000 (2000-02-24) the whole document DOC. AGAINST INV. 71 (SEQ.IDs. 192, 74) --- | 1-14,20, 26,27, 29,30, 35-38 |
| X | DATABASE EMBL 'Online! Accession Number AF046653, 6 April 1998 (1998-04-06) ZAMBROWICZ B. P. ET AL.: "Mus musculus genomic clone OST10140." XP002167969 abstract DOC. AGAINST INV. 76 (SEQ.IDs. 197, 79) --- | 1-4, 6-13,25 |
| P,X | DATABASE EMBL 'Online! Accession Number AF238255, 12 April 2000 (2000-04-12) LIU T. C. ET AL.: "Homo sapiens mixed lineage kinase mRNA." XP002167970 abstract -& LIU T.-C. ET AL.: "Cloning and expression of ZAK, a mixed lineage kinase-like protein containing a leucine-zipper and a sterile-alpha motif." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 274, 11 August 2000 (2000-08-11), pages 811-816, XP002167968 the whole document DOC. AGAINST INV. 77 (SEQ.IDs. 198, 80) --- | 1-14 |
| | --- -/-- | |

INTERNATIONAL SEARCH REPORT

Int. .ional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|--------------------------|
| P, X | WO 00 14212 A (ACTON SUSAN ;MILLENNIUM PHARM INC (US)) 16 March 2000 (2000-03-16) figure 2 DOC. AGAINST INV. 77 (SEQ.IDs. 198, 80) figure 3 DOC. AGAINST INV. 106 (SEQ.IDs. 227, 109) ---- | 1-14, 25-30, 35-38 |
| X | DATABASE EMBL 'Online! Accession Number AA270784, 28 March 1997 (1997-03-28) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:736476." XP002167971 abstract DOC. AGAINST INV. 80 (SEQ.IDs. 201, 83) ---- | 6,7 |
| P, X | PAZDERNIK N. J. ET AL.: "MOUSE RECEPTOR INTERACTING PROTEIN 3 DOES NOT CONTAIN A CASPASE-RECRUITING OR A DEATH DOMAIN BUT INDUCES APOPTOSIS AND ACTIVATES NF-(KAPPA)B" MOLECULAR AND CELLULAR BIOLOGY, vol. 19, no. 10, October 1999 (1999-10), pages 6500-6508, XP000939146 the whole document DOC. AGAINST INV. 80 (SEQ.IDs. 201, 83) ---- | 1-4, 6-13,22 |
| X | DATABASE EMBL 'Online! Accession Number AL031297, 13 August 1998 (1998-08-13) COBLEY V.: "Human DNA sequence from clone 97P20 on chromosome1q23.2-24.3." XP002168227 abstract DOC. AGAINST INV. 81 (SEQ.IDs. 202, 84) ---- | 1-14 |
| X | WO 99 04265 A (SAHIN UGUR ;TURECI OZLEM (DE); PFREUNDSCHUH MICHAEL (DE); GOUT IVA) 28 January 1999 (1999-01-28) SEQ.IDs. 431 and 435 DOC. AGAINST INV. 82 (SEQ.IDs. 203, 85) ---- | 2,6,7, 11,12 |
| X | DATABASE EMBL 'Online! Accession Number AA195964, 28 January 1997 (1997-01-28) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:628136" XP002168228 abstract DOC. AGAINST INV. 84 (SEQ.IDs. 205, 87) ---- | 6,7 |
| | ---- | |
| | -/-- | |

INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|------------------------|
| P,X | <p>DATABASE EMBL 'Online! Accession Number AK000342, 22 February 2000 (2000-02-22) SUGANO S. ET AL.: "Homo sapiens cDNA FLJ20335 fis, clone HEP11429." XP002168229 abstract DOC. AGAINST INV. 84 (SEQ.IDs. 205, 87)</p> | 1-14 |
| X | <p>DATABASE EMBL 'Online! Accession Number AF027406, 6 January 1999 (1999-01-06) BRENNER V. ET AL.: "Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA." XP002168230 abstract DOC. AGAINST INV. 85 (SEQ.IDs. 206, 88)</p> | 1-14 |
| X | <p>DATABASE EMBL 'Online! Accession Number AF043288, 6 January 1999 (1999-01-06) BRENNER V. ET AL.: "Mus musculus muscle-specific serine kinase 1 mRNA." XP002168231 abstract DOC. AGAINST INV. 85 (SEQ.IDs. 206, 88)</p> | 1-4,6-13 |
| P,X | <p>WO 00 22143 A (INCYTE PHARMA INC ;AZIMZAI YALDA (US); CORLEY NEIL C (US); YUE HEN) 20 April 2000 (2000-04-20) SEQ.IDs. 1 and 10 DOC. AGAINST INV. 85 (SEQ.IDs. 206, 88) SEQ.IDs. 7 and 16 DOC. AGAINST INV. 104 (SEQ.IDs. 225, 107)</p> | 1-4, 6-13, 26-28 |
| X | <p>DATABASE EMBL 'Online! Accession Number AI553938, 25 March 1999 (1999-03-25) STAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2090493 3' similar to TR:015367 TSK_1." XP002168388 abstract DOC. AGAINST INV. 86 (SEQ.IDs. 207, 89) DOC. AGAINST INV. 87 (SEQ.IDs. 208, 90) DOC. AGAINST INV. 91 (SEQ.IDs. 212, 94)</p> | 1,2,4-7, 10-14,25 |

-/--

INTERNATIONAL SEARCH REPORT

Int'l Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No |
|------------|---|--------------------------|
| X | <p>DATABASE EMBL 'Online! Accession Number AV040939, 14 May 1999 (1999-05-14) CARNINCI P. ET AL.: "Mus musculus adult male testis cDNA, partial sequence." XP002168389 abstract DOC. AGAINST INV. 87 (SEQ.IDs. 208, 90) ---</p> | 6,7 |
| X | <p>DATABASE EMBL 'Online! Accession Number AA399596, 29 April 1997 (1997-04-29) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:729913 5' similar to TR:G404634 Serine/threonine kinase." XP002168766 abstract DOC. AGAINST INV. 88 (SEQ.IDs. 209, 91) ---</p> | 1,2,4-7, 10-14,25 |
| X | <p>KUENG P. ET AL: "A novel family of serine/threonine kinases participating in spermiogenesis." JOURNAL OF CELL BIOLOGY, vol. 139, no. 7, 29 December 1997 (1997-12-29), pages 1851-1859, XP002168387 ISSN: 0021-9525 the whole document DOC. AGAINST INV. 89 (SEQ.IDs. 210, 92) ---</p> | 1-14, 26-28, 35-38 |
| X | <p>DATABASE EMBL 'Online! Accession Number AI652441, 5 May 1999 (1999-05-05) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2307063 3' similar to TR:P97417 serine/threonine kinase" XP002168390 abstract DOC. AGAINST INV. 89 (SEQ.IDs. 210, 92) ---</p> | 1,2,4-7, 10-14 |
| X | <p>DATABASE EMBL 'Online! Accession Number L77564, 16 June 1996 (1996-06-16) GONG W. ET AL.: "Homo sapiens DGS-G mRNA, 3'-end." XP002168391 abstract DOC. AGAINST INV. 89 (SEQ.IDs. 210, 92) ---</p> | 1,2,4-7, 10-14 |

-/--

INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|--|
| X | <p>DATABASE EMBL 'Online! Accession Number AA905446, 9 April 1998 (1998-04-09) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:1506197 3' similar to TR:P97417 serine threonine kinase." XP002168767 abstract DOC. AGAINST INV. 91 (SEQ.IDs. 212, 9) DOC. AGAINST INV. 86 (SEQ.IDs. 207, 89) ---</p> | <p>1,2,4-7, 10-14,25</p> |
| X | <p>DATABASE EMBL 'Online! Accession Number AI538521, 24 March 1999 (1999-03-24) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2074994 3' similar to SW:UN51_CAEEL Q23023 serine/threonine protein kinase UNC-51" XP002168768 abstract DOC. AGAINST INV. 92 (SEQ.IDs. 213, 95) DOC. AGAINST INV. 93 (SEQ.IDs. 214, 96) ---</p> | <p>1,2,4-7, 10-14,25</p> |
| X | <p>DATABASE EMBL 'Online! Accession Number AA498104, 3 July 1997 (1997-07-03) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:918101." XP002168769 abstract DOC. AGAINST INV. 93 (SEQ.IDs. 214, 96) ---</p> | <p>6,7</p> |
| X | <p>DATABASE EMBL 'Online! Accession Number AA215311, 5 February 1997 (1997-02-05) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:63368 5' similar to TR:E237261 calmodulin-domain protein kinase." XP002168770 abstract DOC. AGAINST INV. 94 (SEQ.IDs. 215, 97) ---</p> | <p>1,2,4-7, 10-14</p> |
| P,X | <p>WO 99 32609 A (KAROLINSKA INNOVATIONS AB ;ZAPHIROPOULOS PETER G (SE); TOFTGAARD R) 1 July 1999 (1999-07-01) SEQ.IDs. 1 and 2 DOC. AGAINST INV. 95 (SEQ.IDs. 216, 98) ---</p> <p style="text-align: center;">-/--</p> | <p>1-14,18, 26-28, 35-38</p> |

INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------|
| X | DATABASE EMBL 'Online! Accession Number AA018361, 10 August 1996 (1996-08-10) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:361543 5' similar to SW:ASK1_ARATH P43291 serine/threonine kinase ASK2." XP002169144 abstract DOC. AGAINST INV. 95 (SEQ.IDs. 216, 98) --- | 1,2,4-7, 10-14,18 |
| X | DATABASE EMBL 'Online! Accession Number AI651075, 5 May 1999 (1999-05-05) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2304078 3' similar to TR:060679 serum inducible kinase." XP002169145 abstract DOC. AGAINST INV. 97 (SEQ.IDs. 218, 100) --- | 1,2,4-7, 10-14,25 |
| X | DATABASE EMBL 'Online! Accession Number W08549, 27 April 1996 (1996-04-27) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:332593." XP002169146 abstract DOC. AGAINST INV. 98 (SEQ.IDs. 219, 101) --- | 6,7 |
| X | DATABASE EMBL 'Online! Accession Number AC002355, 24 July 1997 (1997-07-24) HAWKINS T. L. ET AL.: "Homo sapiens chromosome 9 clone 107G20 map 9q34" XP002169147 abstract DOC. AGAINST INV. 99 (SEQ.IDs. 220, 102) --- | 1-7 |
| X | DATABASE EMBL 'Online! Accession Number AI606679, 26 April 1999 (1999-04-26) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:516008." XP002169148 abstract DOC. AGAINST INV. 100 (SEQ.IDs. 221, 103) --- | 6,7 |
| | --- -/-- | |

INTERNATIONAL SEARCH REPORT

Int .ional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|--------------------------|
| X | <p>DATABASE EMBL 'Online! Accession Number AA493011, 2 July 1997 (1997-07-02) MARRA. M. ET AL.: "Mus musculus cDNA clone IMAGE:917574." XP002169149 abstract DOC. AGAINST INV.100 (SEQ.IDs. 221, 103) ---</p> | 6,7 |
| X | <p>DATABASE EMBL 'Online! Accession Number AA396601, 28 April 1997 (1997-04-28) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:570118." XP002169150 abstract DOC. AGAINST INV.102 (SEQ.IDs. 223, 105) ---</p> | 6,7 |
| E | <p>EP 1 033 401 A (GENSET SA) 6 September 2000 (2000-09-06) SEQ.ID.6560 DOC. AGAINST INV.102 (SEQ.IDs. 223, 105) ---</p> | 2,6,7, 11,12 |
| X | <p>DATABASE EMBL 'Online! Accession Number AA276191, 3 April 1997 (1997-04-03) MARRA M. ET AL.: " Mus musculus cDNA clone IMAGE:776192 5' similar t SW:KRB1_VACCC P20505 30 KD prtein kinase homolog." XP002169151 abstract DOC. AGAINST INV.104 (SEQ.IDs. 225, 107) ---</p> | 1-4,6-13 |
| X | <p>DATABASE EMBL 'Online! Accession Number AA399022, 29 April 1997 (1997-04-29) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:729929." XP002169312 abstract DOC. AGAINST INV.106 (SEQ.IDs. 227, 109) ---</p> | 6,7 |
| X | <p>WO 97 47750 A (IMMUNEX CORP) 18 December 1997 (1997-12-18) the whole document DOC. AGAINST INV.108 (SEQ.IDs. 229, 111) ---</p> | 1-14, 25-30, 35-38 |
| | <p>--- -/--</p> | |

INTERNATIONAL SEARCH REPORT

Int. .ional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------|
| X | <p>DATABASE EMBL 'Online! Accession Number AI298668, 4 December 1998 (1998-12-04) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:1895716 3' similar to SW:NEK1_Mouse P51945 serine/threonine-protein kinase NEK1." XP002169313 abstract DOC. AGAINST INV.108 (SEQ.IDs. 229, 111)</p> | 1,2,4-7, 10-14,25 |
| X | <p>WANG X. S. ET AL.: "MAPKKK6, a novel mitogen-activated protein kinase kinase kinase, that associates with MAPKKK5." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 253, no. 1, 9 December 1998 (1998-12-09), pages 33-37, XP002169311 ISSN: 0006-291X the whole document DOC. AGAINST INV.109 (SEQ.IDs. 230, 112)</p> | 1-14,25 |
| X | <p>DATABASE EMBL 'Online! Accession Number AI638161, 29 April 1999 (1999-04-29) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2239185 3' similar to SW:PAK3_Human 075914 serine/threonine-protein kinase." XP002169314 abstract DOC. AGAINST INV.110 (SEQ.IDs. 231, 113)</p> | 1,2,4-7, 10-14 |
| P,X | <p>NAGASE T. ET AL.: "PREDICTION OF THE CODING SEQUENCES OF UNIDENTIFIED HUMAN GENES. XV. THE COMPLETE SEQUENCES OF 100 NEW CDNA CLONES FROM BRAIN WHICH CODE FOR LARGE PROTEINS IN VITRO" DNA RESEARCH, vol. 6, 29 October 1999 (1999-10-29), pages 337-345, XP000865804 ISSN: 1340-2838 -& DATABASE EMBL 'Online! Accession Number AB033090, 11 November 1999 (1999-11-11) OHARA O. ET AL.: "Homo sapiens mRNA for KIAA1264 protein." XP002169637 abstract DOC. AGAINST INV.110 (SEQ.IDs. 231, 113)</p> <p style="text-align: center;">--- -/--</p> | 1-14 |

INTERNATIONAL SEARCH REPORT

Int. ional Application No

PCT/US 00/14842

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------------|
| X | DATABASE EMBL 'Online! Accession Number H29272, 19 July 1995 (1995-07-19) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:49948." XP002169315 abstract DOC. AGAINST INV.111 (SEQ.IDs. 232, 114) --- | 6,7 |
| P,X | WO 99 64589 A (ZENECA LTD) 16 December 1999 (1999-12-16) the whole document DOC. AGAINST INV.111 (SEQ.IDs. 232, 114) DOC. AGAINST INV.112 (SEQ.IDs. 233, 115) --- | 1-14,23, 26-30, 35-38 |
| X | DATABASE EMBL 'Online! Accession Number AA098024, 27 October 1996 (1996-10-27) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:550913 5' similar to SW:DROME P18475 tyrosine-protein kinase receptor torso precursor." XP002169442 abstract DOC. AGAINST INV.112 (SEQ.IDs. 233, 115) --- | 1-4, 6-13,23 |
| X | DATABASE EMBL 'Online! Accession Number Z98752, 23 August 1997 (1997-08-23) RAMSAY H.: "Human DNA sequence from clone RP1-138B7 on chromosome 20q13.12." XP002169443 nts. 43893 - 62413 DOC. AGAINST INV.113 (SEQ.IDs. 234, 116) --- | 1-14 |
| X | DATABASE EMBL 'Online! Accession Number AF035013, 4 January 1999 (1999-01-04) JIANG Y. AND ZHAO K.: "Homo sapiens cell cycle related kinase mRNA, complete cds." XP002169444 abstract DOC. AGAINST INV.114 (SEQ.IDs. 235, 117) ----- | 1-14,24 |

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/14842

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 31-34
because they do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
1-16 (partially), 17 (completely), 18 and 19 (partially), 20 and 22 (completely), 23-38 (partially)
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:
see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.: 1-16 (partially), 17 (completely), 18 and 19 (partially), 20 and 22 (completely), 23-38 (partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☒ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

A nucleic acid molecule encoding a kinase polypeptide as represented by a 'gene name' selected from 'AA980090', 'AA045601', 'AA297313', 'N23936', '5R72-18-1', '5R79-54-1', '5R65-16-1', 'AA065538', 'H17727', 'W08549', 'AA430250', 'AA139478', 'R87679', 'W65887', 'AA948538', '5R69-23-3', and '5R69-26-2', wherein invention 122 is limited to 'AA980090', invention 123 is limited to 'AA045601', and invention 136 is limited to '5R69-26-2', or a domain thereof; a vector and a recombinant cell comprising said nucleic acid molecule; a nucleic acid probe for the detection of said nucleic acid molecule; a polypeptide encoded by said nucleic acid molecule or a fragment thereof; an antibody or antibody fragment having specific binding affinity to said polypeptide; a hybridoma which produces said antibody; methods for identifying a substance that modulates the kinase activity of said polypeptide; methods for treating a disease or disorder by administering such a substance; and methods for the detection of a said polypeptide.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 31-34

The search was based on the sequence listing furnished in computer readable form, the numbering of which differs from the numbering in the figures.

Claims 31-34 refer to a 'substance that modulates the activity of a kinase' without giving a true technical characterization. Moreover, no such specific compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 5 and 6 PCT). No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/14842

| Patent document cited in search report | Publication date | Patent family member(s) | Publication date |
|---|---------------------|--|--|
| WO 0058473 A | 05-10-2000 | AU 3774500 A | 16-10-2000 |
| WO 0006728 A | 10-02-2000 | AU 5134999 A EP 1100904 A | 21-02-2000 23-05-2001 |
| WO 9858052 A | 23-12-1998 | US 5885803 A AU 8154798 A EP 1007692 A US 6207148 B | 23-03-1999 04-01-1999 14-06-2000 27-03-2001 |
| WO 0055332 A | 21-09-2000 | AU 3899600 A AU 5034200 A WO 0071679 A | 04-10-2000 12-12-2000 30-11-2000 |
| WO 9733909 A | 18-09-1997 | AU 728186 B AU 2329597 A BR 9708082 A CA 2249742 A EP 0914335 A NO 984229 A US 6034218 A | 04-01-2001 01-10-1997 27-07-1999 18-09-1997 12-05-1999 13-11-1998 07-03-2000 |
| WO 9957144 A | 11-11-1999 | AU 3885999 A EP 1075518 A | 23-11-1999 14-02-2001 |
| WO 9811234 A | 19-03-1998 | US 5773699 A US 5863780 A AU 4261197 A EP 0927257 A US 6045792 A US 6232077 B | 30-06-1998 26-01-1999 02-04-1998 07-07-1999 04-04-2000 15-05-2001 |
| EP 0861896 A | 02-09-1998 | DE 19708173 A CA 2224404 A JP 10248566 A | 03-09-1998 28-08-1998 22-09-1998 |
| WO 0035946 A | 22-06-2000 | NONE | |
| WO 9831802 A | 23-07-1998 | AU 6031398 A EP 0972026 A | 07-08-1998 19-01-2000 |
| WO 9950395 A | 07-10-1999 | NONE | |
| WO 9933961 A | 08-07-1999 | AU 1691499 A | 19-07-1999 |
| WO 9801756 A | 15-01-1998 | US 5863729 A AU 3651597 A | 26-01-1999 02-02-1998 |
| WO 9949062 A | 30-09-1999 | AU 3208999 A EP 1073756 A | 18-10-1999 07-02-2001 |
| WO 9835015 A | 13-08-1998 | EP 0972011 A US 5968800 A US 6030788 A | 19-01-2000 19-10-1999 29-02-2000 |
| WO 9938981 A | 05-08-1999 | US 5962232 A AU 2113899 A EP 1051497 A | 05-10-1999 16-08-1999 15-11-2000 |

Form PCT/ISA/210 (patent family annex) (July 1992)

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/14842

| Patent document cited in search report | | Publication date | Patent family member(s) | Publication date |
|---|---|---------------------|----------------------------|---------------------|
| WO 9836054 | A | 20-08-1998 | AU 5973498 A | 08-09-1998 |
| WO 9958558 | A | 18-11-1999 | AU 4077099 A | 29-11-1999 |
| | | | EP 1078057 A | 28-02-2001 |
| US 6013455 | A | 11-01-2000 | AU 1315900 A | 01-05-2000 |
| | | | WO 0022143 A | 20-04-2000 |
| EP 0870825 | A | 14-10-1998 | US 5965420 A | 12-10-1999 |
| | | | CA 2231046 A | 05-09-1998 |
| | | | JP 11000179 A | 06-01-1999 |
| | | | US 6165766 A | 26-12-2000 |
| WO 9405794 | A | 17-03-1994 | EP 0658204 A | 21-06-1995 |
| | | | US 5690930 A | 25-11-1997 |
| WO 0009678 | A | 24-02-2000 | AU 5491599 A | 06-03-2000 |
| WO 0014212 | A | 16-03-2000 | US 6183962 B | 06-02-2001 |
| | | | AU 5817799 A | 27-03-2000 |
| | | | US 6043040 A | 28-03-2000 |
| | | | US 6146841 A | 14-11-2000 |
| | | | US 6180358 B | 30-01-2001 |
| | | | US 6153417 A | 28-11-2000 |
| | | | US 6146832 A | 14-11-2000 |
| | | | US 6190874 B | 20-02-2001 |
| | | | US 6121030 A | 19-09-2000 |
| | | | US 6200770 B | 13-03-2001 |
| | | | US 6214597 B | 10-04-2001 |
| WO 9904265 | A | 28-01-1999 | US 6218521 B | 17-04-2001 |
| | | | US 6043084 A | 28-03-2000 |
| | | | AU 8571598 A | 10-02-1999 |
| | | | EP 0996857 A | 03-05-2000 |
| WO 0022143 | A | 20-04-2000 | US 6013455 A | 11-01-2000 |
| | | | AU 1315900 A | 01-05-2000 |
| WO 9932609 | A | 01-07-1999 | AU 1991799 A | 12-07-1999 |
| | | | AU 1991899 A | 12-07-1999 |
| | | | EP 1037920 A | 27-09-2000 |
| | | | WO 9932517 A | 01-07-1999 |
| EP 1033401 | A | 06-09-2000 | NONE | |
| WO 9747750 | A | 18-12-1997 | AU 718792 B | 20-04-2000 |
| | | | AU 3284297 A | 07-01-1998 |
| | | | EP 0914451 A | 12-05-1999 |
| | | | JP 2000512147 T | 19-09-2000 |
| | | | NO 985742 A | 10-02-1999 |
| WO 9964589 | A | 16-12-1999 | AU 4278299 A | 30-12-1999 |
| | | | EP 1084245 A | 21-03-2001 |

4